STIC-Biotech/ChemLib

From:

Sent: To: Subject: Chan, Christina

Wednesday, May 10, 2006 5:46 PM Graser, Jennifer; STIC-Biotech/ChemLib

RE: rush search

Please Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

-----Original Message-----

From: Sent:

Graser, Jennifer

To:

Wednesday, May 10, 2006 5:46 PM Chan, Christina rush search

Subject:

Importance: High

Hi Christina,

Will you please authorize the following rush search a special case which is due?

Thanks.

Jennifer

STIC:

Please search nucleotides 11357 to 12736 of SEQ ID NO: 35 from application 10/672787 in pending and commercial databases.

Thanks, Jennifer Graser Primary Examiner Art Unit 1645 **REM 3B09**

2-0858

Na 96109

Searcher: Searcher Phone: Date Searcher Picked up: Date completed: Searcher Prep Time: Online Time:

Type of Search AA#: Oligomer: Encode/Transl: Structure #: Text: Inventor: Litigation: Vendors and cost where applicable STN: DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS: SEQUENCE SYSTEM: WWW/Internet: Other (Specify):

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Maximum Match 100%
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1 (bases 1 to 96109)

Lagace, R. E., Patterson, C. and Berg, K. L.

Nucleic acids encoding 3-ketoacyl-ACP reductase from Moraxella

Catarrahalis

Patent: US 6612636-A 35 14-OCT-2003;

Elitra Pharmaceuticals Inc.; San Diego, CA

Location/Qualifiers
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1 TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGG [/organism="unknown" /organism="unknown" /mol_type="genomic DNA" Db 432	d	97 721 1410 bp DNA linear PAT 20-FEB-2004 Db 672 150009 161:42679066 27 Db 612 28 Db 612	Oy 1261 ATCTGCCAAGGTAGGATTGGGATTGACCATCGATGATGCTAACCTTTGTGACCGTGATTGAC 1320 B52 TT	1247) GEGEGEACHARIAC I GEGETIC I 1993 I MATECCEGEGE IGATEM I GRACE 12336 QY 1201 TGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGAACAATGAACGCCTGTGGGCAGTTT 1260 Db 912	1081 TGCTTYGAGTGTAYCAACCAATTGAACATCGCTGAYCACAGGAATGCCTTGAGGTTY 1140 1082	12317 ĠACACCAACAATCATĠCCTĠCATĠTTTTĠCCCATCCTCCCTACTAATĠTCGTAACAĠTĠCT 12376 1021 TITGGCATTTGAGCCTGTGATGGCGATGATTGGTGTTTTGTTGGTTG		781 CAAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGCGGAGAGATTTAAAATTGT 840	
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                                                                             GCTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGAACGAATGAACGCCTGTGGGCAGT 1258
                                                                                                                                                                                                                          CGTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCT
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                                      ATTGCTGCAATGGTTGAGCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTA
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109265 GCAATTGTGGCGACATATTGGCAGCGATGCTCAAGACCTGCAAACTGCTGCAAGGTGCTA 109324
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Breton, G. and Bush, D.
Nucleic acid and amino acid sequences relating baumannii for diagnostics and therapeutics patent: US 6562958-A 1282 13-MAY-2003;
Genome Therapeutics Corporation; Waltham, MA Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                      1 TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC
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Pasteurellaceae; Haemophilus.
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                                                                                                                       CTGCATAACATATGCTGACAGCTCACTAAAATCTTGACCTTTACCAAAGCCCCAAAAT
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                                   CAAATGCAATTTACCCTCAATATA------AAGCCCAGCCAATGCAGCAACTGTACT
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  -TATCTTCATTGTTCAACACACCTACTTTAGCATTATGATAAATGCGTAATTTTGCTT
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VERSION
KEYWORDS
SOURCE
ORGANISM
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Best Local Similarity 49.6%;
Matches 683; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9122 TAAACATTGAGCTAAATGCGTAAATTCTTCGCCGCGCTTTTCAAAAGAAGCAAACTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9062 GAGACTTGCACAAGCAGGCGACAATAATACCA-----TATCTCCGCTTTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CATGCTAGCACAAGCAGGTGACAAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA
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Location/Qualifiers
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Haemophilus influenzae
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Iversen, P.L.
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                                                                                                                                                                                                                                                                                                                                                                                                      AAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAGGTTATGCTTGCC
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TGGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTTTTCAAAAATACGCAATTTTTGTG
                                                      CGCTTGATTTTCGTTTTCCCCAAAAGTCAGCC
                                                                                                       TGATAATGGTGTGATTTGGGGCAACGCTTGTCAGTGTGGTCAAGCATTGCTTGGCTAAAT
                                                                                                                                                        GCCATTTTCAGTTTTTAGCCAATAATCCGCACTATTTTCCGCAAAAAGAAACGGTATGTTT
                                                                                                                                                                                                                                                                AACCAATGTAGCTTCTTCACAAGGTAAAATCACTTCATCTTTTACCATTAAATATTGCTT
                                                                                                                                                                                                                                                                                                              AATACCTATAGCTTGTGCCAATGCTGTTGCTGCCAAAATGTTCATATAATTATGGCGACC
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/organism="Haemophilus influenzae"
/mol_type="unassigned DNA"
/db_xref="taxon:727"
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Pred. No. 1.9e-40;
0; Mismatches 606;
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1020 TTTGCCATTGAGCCCTGTAGGCCATGATTGGTGTTTGTTGCTTGAGTTAGATCTC 1079	Length 110000; Indels 89; Gaps 7; TATAATTTTAAATTGATC 60 Oy	Query Match 11.6%; Score 160.4; DB 2; Length 110000; Best Local Similarity 49.6%; Pred. No. 3e-40; Matches 683; Conservative 0; Mismatches 606; Indels 89; Gaps Oy 1 TAAAGCGTGAACCATGTTAACAACTTATCACCTCGCTCATTATAATTTTAAATTGATC
960 CGACACCAACAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACAGTGC 1019	(BD426631 The Nucleotide Sequence Db	1600001 1710000 1700001 1810000 1800001 1830121 of 19) of BD426631 from base 1100001
900 CCACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGGCGTGCCAATATTACCGC 959	Qy da	B0426631 12 120000 1310000 B0426631 13 130000 1410000 B0426631 14 140000 1510000 B0426631 15 150000 1610000
840 TTGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCA 899	Qy Db	800001 9 900001 10 1000001 11
780 CCAAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGCGGAGAGATTTAAAATTG 839	Оу	400001 500001 600001
720 TGGCATCGTCTGGGTAGATGATGGCGGTTTGGCAATTTTCAAAAATACGCAATTTTTGTG 779	Qy dd	100001 200001 300001
660 TGATAATGGTGTGATTTGGGGGAACGCTTGTCAGTGTGGTCAAGCATTGCTTGGCTAAAT 719	Oy Db	BD426631 11/c BD426631 11/c WPCOMMENT Sequence split into 19 fragments LOCUS BD426631 Accession Fragment Name Regin End
601 ATCACCATCAAATAAATAAAAATCTGC-CGTTTGGTGGCTAAGTAAGCTATTTGTTG 659	ĠĀTĀGTĀATĀTTĪT 7833 Qy	Db 7890 AGAGATAATCCACACAAGAAAGACCTGTTTTGCCAAGCCCGATGATAGTAATATTTTT
541 TTTGATTTTAATTGATGGATGGTAAAAGTTTGTTTTTTTGATGA	ATTAGCCTGTTGGGATÄ 7891 Qy GACGGCATATTTTTT 1377 Db	Db 7950 TATCAATACCAGTAGGATTTTTTCGAGTATCAATCACACGAATATTAGCCTGTTGGGATA OY 1320 CCAAAAAATTCACAGGCTGACAGTCCAGAGCTGCCCAAACCGACGACGGCATATTTTTT 1
	1319	1260
104046 TTGAAAACGATGATCTAACCCTTTGAAATGACGAAGTGCGGTACGAATTGAATCTAAATT 103987 481 AAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTTATGCTTGCC 540	AACGCCTGTGGGCAGTT 1259	QY 1200 CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGAACAGCCCTGTGGGCAGTT
104106 CCCCACATITIGITIGCTITIAGAGTCATIAATCCAACGAATGCCATTAGCTTGATGCACTAA 10404/ 421 TTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGGGTATCAAGCATGGCATCCATGGG 480	AATAACAATCATATCGC 8011 Qy	DS 8070 GTGCGGTTTGAATTTCTGGTGTTTTTACCGCAAGCCCTGGGCTAATAACAATCATATCGC
361 GCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCAATATA 420	8071	8111
301 CAATGCCAGTGATATATGCCATAAACCGTGCCAAGCCCATCAATTGCTGCAATGGTTGA 360	TGCGCGGCA 8112 Qy AGGAATGCCTTGAGCTT 1139 Db	Db 8163 TTTTACCATTTGAACCTGTAATCCCCACAATTGGCTTTGTCGCTGCGCGCA QY 1080 GTGCTTTGAGTGTATCAATGAACATTGAACATTGGCTTTGTCACAGGAATGCCTTGAGCTT
241 CTGCATAACATATGCTGACAGCTCACTAAAATCTTGACCTTTACCAAGCCACCCAAAAT 300 	TAAAGTAGTTAGGTAC 8164 QY TGCTTGAGTTAGATCTC 1079 Db	QY 1020 TITTGGCATTICACACCAGCAGCATGCTTCGCCATTTCATAAACTAAAGTAGTTAGATCTC QY 1020 TITTGGCATTTGAGCCTGTGATGGCGATGATTGGTGTGTTTGTT
104277 CGATGAAAATTTTGCAAGCAGCGCACCATCTCGACCAAAACAATAACAAATAATGTGTGG 104218	ATGTCGTAACAGTGC 1019	960
104331 TGTTGGGCGTAAAAATTCTATCGCTTGTTCCATTGTATCGAACAAALAACTTTG 104278 181 GAGTAAATCTTGGCTCAATTATCGGGGGATCTTGACCGATTAAATACACACTATCCACCCA 240	GCGIGCCAATATIACCGC 959	Db 8280 CATAAAGTTCACAATCTTCATTCAACAATGACAAAAGCGGGAATCCCAATATTCCGC
	8281	8340 H
61 CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA 120	AGTCACGTTCAAGACAG 8341 Qy ACTTGACAGCTCAAGCA 899 Db	Db 8400 GGCGATAATCTTCTAAATCCATATAGCGATCCATATGATCTTCAGTCACGTTCAAGACAG Qy 840 TIGCCCCTTGAGCTGCCAAAITTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCA
		780 CCAAATAA

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Fragment Name BD426631 00 BD426631 03 BD426631 04 BD426631 06 BD426631 07 BD426631 09 BD426631 10 BD426631 10 BD426631 11 BD426631 11 BD426631 13 BD426631 13 BD426631 15 BD426631 16 BD426631 17 BD426631 18 BD426631 18 BD426631 17 BD426631 18 BD426631 BD42663
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Matches 683; Conservative
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Best Local Similarity 49.6%;
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                                                     CAATGCCAGTGATGATATGCCATAAACCGTGCCAAGCCCATCAATTGCTGCAATGGTTGA 360
                                                                                                                                    GAGACTTGCACAAGCAGGCGACAATAATACCA----TATCTCCGCTTTGCAA
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                                                                                                                                                                                              CGATGAAAATTTTGCAAGCAGCGCACCATCTCGACCAAAAACAATAACAAATAATGTGTGG
                                                                                                                                                                                                                         GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA
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                                                                                                           TTGATTAATTCAGCTAATTCTGAAAAATCAGCCCCTTTTCCGTCTCCGCCTAGCAA
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Pred. No. 3e-40;
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Best Local Similarity 49.6%;
Matches 683; Conservative
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CGCTTGATTTTCGTTTTCCCCAAAAGTCAGCC-
                                                      GCCATTTTCAGTTTTTAGCCAATAATCCGCACTATTTTCCGCAAAAGAAACGGTATGTTT
                                                                                                            AACCAATGTAGCTTCTTCACAAGGTAAAATCACTTCATCTTTTACCATTAAATATTGCTT
                                                                                                                                     AAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAGGTTATGCTTGCC
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                         TGATAATGGTGTGATTTGGGGCAACGCTTGTCAGTGTGGTCAAGCATTGCTTGGCTAAAT
                                                                               ATCACCATCATCAAATAAATAAAATCTGC-CGTTTGGTGGCTAAGTAAGCTATTTGTTG
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1140 TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGG
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                                                      CCAAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGACGCATATTTTT 1377
                                                                                                                                                                              TATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGATTGA 1319
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AGAGATAATCCACACAAGAAGACCTGTTTTGCCAAGCCCGATGATAGTAATATTTT 103150
                                                                                                                                                                                                                                                                                                           CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGCAGTT
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                                                                                                                       TATCAATACCAGTAGGATTTTTTCGAGTATCAATCACACGAATATTAGCCTGTTGGGATA 103208
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Sequence split into 19 fragments LOCUS AR274513 Accession AR274513

Fragment Name Begin End
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AR274513_01 100001 210000
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AR274513_03 300001 410000
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Continuation (13 of 19) of AR274513 from base 1200001 (AR274513 Sequence 1 from Query Match 11.6%; Score 160.4; DB 2; Length 110000;

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TTTTGGCATTTGAGCCTGTGATGGCGATGATTGGTGTGTTTTGTTGTTGAGTTAGATCTC
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                                                                                                 GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA
                                                                                                                                     TGTTGGGGCGTAAAAATTCTATCGCTTGTTCCATTGTATCGAACAA-----ATAACTTTG
                  TTGATTAATTTAATTCAGCTAATTCTGAAAAATCAGCCCCTTTTCCGTCTCCGCCTAGCAA 10415
                                                                            CGATGAAAATTTTGCAAGCAGCGCACCATCTCGACCAAAACAATAACAAATAATGTGTGG
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Fragment Name
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AR632719 02
AR632719 03
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            AGAGATAATCCACACAAGAAAGACCTGTTTTGCCAAGCCCGATGATAGTAATATTTTT
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                                                CCAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGACGCATATTTTTT
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                                                                                         TATICAATACCAGTAGGATTTTTTCGAGTATICAATCACGACTATTAGCCTGTTGGGATA 103208
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2: geneseqm2000
3: geneseqm2001
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6: geneseqm2002
7: geneseqm2002
8: geneseqm2003
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11: geneseqm200
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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152.8	157.6 154.4 152.8	160.4 160.4 160.4	231 226.2 160.4 160.4	1380 1380 1370.4	Score
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110000	110000 110000 14324 349980 1281	1314 110000 110000	1344 1416 1314 1314	1398 96109 1410	% Query Match Length
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WPI; 2003-029926/02. P-PSDB; ABU35455.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

The invention relates to an isolated nucleic acid comprising any one of

Claim 14; SEQ ID NO 27195; 1766pp; English.

Wang L, Wall D,

Malone C, Carr GJ,

Haselbeck R, Yamamoto R,

Ohlsen Forsyth

Z (Z

Zyskind JW; Xu HH;

(ELIT-) ELITRA PHARM INC. Zamudio C, Trawick JD,

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107. 107. 1093. 1093. 1093.			٢		1398		00 00											4.0		•			44		14	
Q O _J	essential gene; cell p	#20982.			BP.	ALIGNMENTS	ACA51965 ACA35530	AAS56341	ACF6/36/_48	ACF71682	ACA43846	AAS89273	AAS89816	ACA51133	NAZ47131	ABD09257	ABD09098	AAS54275	ACA45658	ACA44759	ли	AAH81460	AAS52295	ט מ	087	
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid cencoding a polypeptide whose expression is inhibited by the antisense curve in the acid; (2) a host cell containing the vector; (3) an isolated collected collected collected by the antisense curve in the acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular colliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits proliferation of the biological pathway in which a proliferation-required gene or its gene product lies cor a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene conduct is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the condition of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational crequired for proliferation in cells other than S. aureus, S. typhimurium, C. pneumoniae or P. aeruginosa. The present sequence is one of the target creation, in full cassential genes. Note: The sequence is one of the target creation, in the printed specification, but was obtained in cells one of the printed specification, but was obtained in
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Moraxella catarrhalis.

bronchopulmonary;

Genomic library; bacteria; human upper airway; otitis media;

sinusitis;

endocarditis; meningitis;

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16-JUN-2000; 28-DEC-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic acids.
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                                                                                                                                                       GCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATCAATATA
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                            AAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAGGTTATGCTTGCC
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RESULT 3
ADL02987/c
ID ADL029
XX ADL 06-MAY-2004 Moraxella ADL02987; ADL02987 DNA encoding a M. catarrhalis protein #673 gene; Moraxella catarrhalis; infection standard; (first entry) DNA; 1410

06-JAN-2004



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P-PSDB; ADL04907.
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                                                                                                                                                                                                                                                                                                                                                                                                           cc encoding a polypeptide whose expression is inhibited by the antisense cc nucleic acid; (2) a host cell containing the vector; (3) an isolated co polypeptide or its fragment whose expression is inhibited by the cc polypeptide; (6) producing the polypeptide; (6) inhibiting cellular cc antisense nucleic acid; (4) an antibody capable of specifically binding ct the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for cc proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway conceptive for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the compound that inhibits are useful for identifying proteins or screening for homologous nucleic acids are useful for collection of an organism. The antisense nucleic acids required conditions of collection of an organism, or for screening homologous nucleic acids required conditions of collection in cells other than S. aureus, S. typhimurium, C. pneumoniae or P. aeruginosa. The present sequence is one of the target convolution of the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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08-FEB-2002;
06-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1) a vector comprising a promoter operably linked to the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e invention relates to an isolated nucleic acid comprising any one of e 6213 antisense sequences given in the specification where expression the nucleic acid inhibits proliferation of a cell. Also included are:
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late candidate molecules for rational drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antisense nucleic acids, useful for identifying proteins or screening homologous nucleic acids required for cellular proliferation to
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     GTTGACACAGCTCGACAGCTTCTTTAAGCGTTGCTGCATGTAAAATTTTAGTTGCGCCT-
                                                                                                                                                   ACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTTG 181
                                                                                                                                                                                     AAACTTGCACATGCTGGTGAT-----AGCAATACCACATCTTCAGCTTGTGTTTCAC 122
                                                                                                                                                                                                                      ATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAAT
                                         AACGAATTGACGCAGGCAACAAACTGCTGACCACGGTCATTATAACTTTTAAACATATCA
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                                                                                                                                                                                                                                                                                                                                                                                                        BP; 385 A; 254 C; 318 G; 387 T; 0
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TTGACCAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGACGACGATAT 1372
                                                      ATCTGATCGTGTCCGGGAGGTGTGGGGGCGGGAGTCCGTTACAGCAACTTGGTAGCCTTGT
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                                                                                        AGTTTATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGA 1315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
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                                                                                                                                                                                                                   CC The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the genes, CC their use in the discovery of novel antibiotics, the essential genes CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, CC pseudomonas aeruginosa and Enterococcus faecalis. The invention is also CC useful for the identification of potential new targets for antibiotic CC development. The antisense nucleic acids can also be used to identify CC proteins used in proliferation, to express these proteins, and to obtain CC antibodies capable of binding to the expressed proteins. The proteins can CC used to screen compounds in rational drug discovery programmes. The used to serve nucleic acids sequence is also useful to screen for homologous CC antisense nucleic acids sequence is also useful to screen for homologous culleic acids which are required for cell proliferation in a wide variety CC of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent CC did not form part of the printed specification, but was obtained in CC electronic format directly from WIPO at
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 the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; ds; prokaryotic essential
                                                                                                                                                                                                               antisense nucleic acids, useful for identifying proteins or screening homologous nucleic acids required for cellular proliferation to late candidate molecules for rational drug discovery programs.
                                                                                                                                                                 invention relates to an isolated nucleic acid comprising any
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CC or a gene on which the test compound that inhibits proliferation of an CC organism acts; (9) manufacturing an antiblotic; (10) profiling a CC compound's activity; (11) a culture comprising strains in which the gene CC compound's activity; (11) a culture comprising strains in which the gene CC product is overexpressed or underexpressed; (12) determining the extent CC strains; or (13) identifying the target of a compound that inhibits the CC proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required CC for cellular proliferation to isolate candidate molecules for rational CC drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, CC required for proliferation in cells other than S. aureus, S. typhimurium, CC prokaryotic essential genes. Note: The sequence data for this patent did cot form part of the printed specification, but was obtained in CC electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1308 TAAACATTGAGCTAAATGCGTAAATTCTTCGCCGCGCTTTTCAAAAAGAAGCAAACTGATC
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                                                                                                                                                                                                                                                                                               UDP-N-acetylmuramylalanyl-D-glutamate-2-6-diaminopimelate ligase; D-alanine-D-alanine adding enzyme; D-alanine-D-alanine ligase; UDP-N-acetylpuyruvoylglucosamine reductase; UDP-N-acetylglucosamine pyrophosphorylase; UDP-N-acetylmuramoylalanine-D-glutamate ligase; DP-N-acetylmuramoylalanine ligase; aspartate semialdehyde dehydr UDP-N-acetylmuramoylalanyl-D-glutamate; X-ray diffraction analysi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; gene; antibacterial;

UDP-N-acetylglucosamine 1-carboxyvinyl transferase;

CTP:CMP-3-deoxy-D-manno-octulosonate transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL46439
      08-APR-2002; 2002US-0370899P
                                                              08-APR-2003; 2003WO-CA000481
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diffraction analysis.
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cc at least one activity of specified bacterial enzymes involved in cell cmembrane biogenesis. (I) are: UDP-N-acetylglucosamine 1-carboxyvinyl cransferase-1 of Streptococcus pneumoniae (S.p), Pseudomonas aeruginosa (P.a.) or Staphylococcus aureus (S.a.); CTP:(CMP-3-deoxy-D-manno-cculosonate transferase of Escherichia coli (E.c.) or Haemophilus (influenzae (H.i.); UDP-N-acetylmuramylalanyl-D-glutamate-2,6-cc diaminopimelate ligase of Escherichia coli (E.c.) or Haemophilus (C or P.a.; D-alanine-D-alanine ligase of Enterococus faecalis (E.f.); UDP-N-acetylglucosamine pyrophosphorylase of E.f., H.i. or S.a.; UDP-N-acetylmuramylalanine-D-glutamate ligase of E.f., or H.i.; UDP-N-acetylmuramoylalanine-D-glutamate ligase of E.f. or H.i.; DP-N-acetylmuramoylalanine-D-glutamate by S. acetylmuramoylalanine-D-glutamate ligase of E.f. or H.i.; DP-N-acetylmuramoylalanine-D-glutamate ligase of E.f. or H.i.; DP-N-acetylmuramoylalanyl-D-glutamate ligase of E.f. or H.i.; DP-N-acetylmuram
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Best Local S
Matches 683
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24-DEC-2002;
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27-DEC-2002;
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09-APR-2002;
09-APR-2002;
31-MAY-2002;
06-JUN-2002;
01-AUG-2002;
06-NOV-2002;
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Beattie
Virag C,
                                                                                                                                                                                                                                                                                                                                  Sequence 1314 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant bacterial enzymes involved in cell membrane useful for designing potential antibacterial agents.
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                                                                                                                                                                                                       1 TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC
                                                                                                                                                                                                                                                                                                                                                                        invention.
                                                                                                                                                                                                                                                                   Similarity
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                                                                               GAGACTTGCACAAGCAGGCGACAATAATACCA-----TATCTCCGCTTTGCAA
                                                                                                                                                                 TAAACATTGAGCTAAATGCGTAAATTCTTCGCCGCGCTTTTCAAAAGAAGCAAACTGATC
TGTTGGGCGTAAAAATTCTATCGCTTGTTCCATTGTATCGAACAA---
                                      TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTT
                                                                                                                        CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA
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; 2002US-0436893P.
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; 2002US-0437013P.
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2002US-0436345P
2002US-0436349P
2002US-0436569P
2002US-0436569P
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2002US-0436734P
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2002US-0371107P.
2002US-0371185P.
2002US-0385426P.
2002US-0385426P.
2002US-0400348P.
2002US-04003495P.
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                                                                                                                                                                                                                                                                                                                               403 A;
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Ouyang H,
Pinder B,
                                                                                                                                                                                                                                                                                                                             214 C; 294 G;
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                                                                                                                                                                                                                                                Score 160.4; | Pred. No. 2.4e | 0; Mismatches
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Vallee F, Richards D,
Alam MZ, Tai M, Canad
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  --ATAACTTTG
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GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA

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1260 TATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGATTGA
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                                                     TTTCAAGTAACCATTCCTGATTTAAACTACCAGTATGAAGAGGGATATTTTGAGGAAGTT
                                                                                                                    GTGCGGTTTGÄÄTTTCTGGTGTTTTTÄCCGCÄÄGCCCTGGGCTÄÄTÄÄCÄÄTCÄTÄTCGC
                                                                                                                                     TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGG
                                                                                                                                                                                                      GTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTT
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                                                                                CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGCAGTT
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PYOTE 10-AUG-2005.

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US2005181388-A1.

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PYOTE 10-AUG-2005.

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18-AUG-2005.

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18-AUG-2002; 2002US-PR

04-APR-2002; 2002US-PR

05-AUN-2002; 2002US-PR

06-APR-2002; 2002US-PR

06-JUN-2002; 2002US-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sin purification; antibacterial; antimicrobial; infection;
screening; gene; ds; UDP-N-acetylmuramoylalanine-D-glutamate ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 TATCAATACCAGTAGGATTTTTTCGAGTATCAATCACACGAATATTAGCCTGTTGGGATA 77
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  2002US-0370859P.
2002US-0370859P.
2002US-03709159P.
2002US-0371140P.
2002US-0371140P.
2002US-0385426P.
2002US-03863618P.
2002US-03863618P.
2002US-0386367P.
2002US-0386367P.
2002US-0386367P.
2002US-0386369P.
2002US-0386869P.
2002US-0386869P.
2002US-0386869P.
2002US-0386869P.
2002US-0386869P.
2002US-0386869P.
2002US-0386869P.
2002US-0386869P.
2002US-0386869P.
2002US-0424399P.
2002US-0424369P.
2002US-0436349P.
2002US-0436568P.
2002US-0436568P.
2002US-0436768P.
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2002US-0436768P.
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2002US-0370792P.
2002US-0370820P.
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                                                                                                                                                                                                                    Query Match
Best Local S
Matches 683
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27-DEC-2002;
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Beattie
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                                                                                                                                                                                                                                                                                           Sequence
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                                                                      GAGACTTGCACAAGCAGGCGACAATAATACCA
                                                                                                                                           TAAACATTGAGCTAAATGCGTAAATTCTTCGCCGCGCTTTTCAAAAGAAGCAAACTGATC
TGTTGGGCGTAAAAATTCTATCGCTTGTTCCATTGTATCGAACAA----
                                TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTT
                                                                                                           CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA
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Buzadzija K, Canadien
D, Li Q, Mansoury K,
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2002US-0436843P.

2002US-0436861P.

2002US-0436885P.

2002US-0436889P.

2002US-0436990P.

2002US-0436997P.

2002US-043697P.

2002US-043697P.

2002US-043697P.

2002US-043791P.

2002US-043791P.

2002US-043791P.

2002US-043791P.

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2002US-043753P.

2002US-043753P.

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2003WO-CA000464.

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49.6%;
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RESULT 10

AAT42063 11/c

AAT42063 11/c

Continuation (12 of 19

WP Sequence split intc

WP Fragment Name

WP AAT42063 00

WP AAT42063 03

WP AAT42063 03

WP AAT42063 06

WP AAT42063 06

WP AAT42063 07

WP AAT42063 07

WP AAT42063 10

WP AAT42063 10

WP AAT42063 11

WP AAT42063 11

WP AAT42063 13

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                                                     TTGAAAACGATGATCTAACCCTTTGAAATGACGAAGTGCGGTACGAATTGAATCTAAATT
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RESULT 11

AAT42063 12/c

AAT42063 12/c

Continuation (13 of 19

WP Sequence split into
WP Fragment Name
WP AAT42063 00

WP AAT42063 02

WP AAT42063 03

WP AAT42063 04

WP AAT42063 06

WP AAT42063 06

WP AAT42063 07

WP AAT42063 07

WP AAT42063 09

WP AAT42063 09

WP AAT42063 09

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                                                                                                                    TGGCATCGTCTTGGTAGATGATGACGCGTTTGGCAATTTTCAAAAATACGCAATTTTTGTG
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                 TIGCCCCTIGAGCIGCCAAATITGAGATAIGCICAAGCIGAAAACTIGACAGCICAAGCA
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Pred. No. 1.3e-33;
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Best Local Similarity 51.9%;
Matches 467; Conservative
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GCGCGTCTTTGCCAAAAGAGATGCATTTTATATCTGCTTGACAGGATTGGTGAGGA----
         CTATTTGTTGTGATAATGGTGGATTTGGGGCAACGCTTGTCAGTGTGGTCAAGCATTGC
                                AAATAAATAGTATTCTCTTGTTCAATCAGCCCCCAATTTCCCCATT
                                          TGTTGCATAGAAATTCCCGCTGCTTCGGCTAAAGCACAAGCAGCAGCGCATTCATCCAA
                                                                                                         GCATCCATGGGAAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAGG
                                                                                                                               TCTCTTACCCACTGACATCGATGTGGCAGTCCAGGGAAGGTTTTTAAAAACATTAAGAATG
                                                                                                                                         TCATCAATATATTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGGGTATCAAGCATG
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                           Query Match
Best Local Similarity
Matches 591; Conserv
                                                                                                                                               The invention comprises nucleotide sequences (genes) from the genome of nontypeable strain of Haemophilus influenzae (NTH1). The NTH1 DNA sequences of the invention are useful for treating or preventing NTH1 bacterial infections of the middle ear and/or nasopharynx. The present nucleic acid represents an NTH1 contig sequence of the invention.
                                                                                                                                                                                                                                                                                                                                New polynucleotides of nontypeable strain of Haemophilus influenzae, useful for treating or preventing NTHi bacterial infections of the mear and/or nasopharynx.
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                                           CATATCCCTTTCAAGTAACCATTCCTGATTTAAACTACCAGTATGAAGAGGGATATTTTG
                                                                                 CTGATCGGCTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGT
                                                                                                                               CGCTTTAAGTGCGGTTTGAATTTCTGGTGTTTTTACCGCAAGCCCTGGGCTAATAACAAT
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Matches 591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 349980 BP; 105127 A; 63538 C; 70035 G; 111276 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides of nontypeable strain of Haemophilus influenzae, useful for treating or preventing NTHi bacterial infections of the middle ear and/or nasopharynx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 685; 88pp; English
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REFERENCE AUTHORS TITLE VERSION KEYWORDS SOURCE ORGANISM RESULT 1
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ACCESSION Ś S 밁 Ś 밁 밁 Ś ORIGIN FEATURES Query Match 100.0%; Score 1380; Best Local Similarity 100.0%; Pred. No. 0; Matches 1380; Conservative 0; Mismatches JOURNAL 11477 11417 11357 181 61 CATGCTAGCACAAGCAGGTGACAAAAGCACAGGCCCTAGCGGTGCTTTGACTGGCTGCCAA 120 AR408756 Sequence 35 AR408756 1 TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC Patent: US 6632636-A 35 14-OCT-2003; Elitra Pharmaceuticals Inc.; San Die Location/Qualifiers 1 (bases 1 to 96109)
Lagace, R.E., Patterson, C. and Berg, K.L.
Nucleic acids encoding 3-ketoacyl-ACP reductase from catarrahalis Unknown. Unclassified. Unknown. AR408756.1 GAGTAMATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA 11596 GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTT TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTT CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC 1. .96109 /organism="unknown"
/mol_type="genomic | 96109 bp from patent US 6632636. GI:40159151 San Diego, DNA В 0, 6, Ç Length 96109; Indels linear PAT 18-DEC-2003 0; Gaps 180 60 11536 11476 11416 0

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601 ATCACCATCAAATAAATAAAAATCTGCCGTTTGGTGGCTAAGTAAG	541 TTTGATTTTAATTGATGGATTGGTAAAAGTTTGTTTTTTT	481 AAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAGGTTATGCTTGCC 540 	421 TTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGGGTATCAAGCATGGCATCCATGGG 480	361 GCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATCAATATA 420 	301 CAATGCCAGTGATGATATGCCATAAACCGTGCCAAGCCCATCAATTGCTGCAATGGTTGA 360	241 CTGCATAACATATGCTGACAGCTCACTAAAATCTTGACCTTTACCAAGCCCACCCA	181 GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA 240	121 TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTT 180	61 CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA 120	1 TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAAATTTTTAAATTGATC 60 	y Match 100.0%; Score 1380; DB 6; Length 96109; Local Similarity 100.0%; Pred. No. 0; hes 1380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		1321 CAAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGACGCATATTTTTTTGA 1380

JOURNAL FEATURES SOUR ORIGIN	VERSION KEYWORDS SOURCE ORGANISM REFERENCE REFERENCE AUTHORS	RESULT 3 AR450009/c LOCUS DEFINITION ACCESSION	D 90 B	Qy Db	8 B 8	40 40 40 40	\$ & B	୧୫୧	B & B &	Qy da	B &	Db
ANCIEL CACID AND AMINO ACID SEQUENCES PELATING TO M. CATAITHALIS for diagnostics and therapeutics RNAL Patent: US 6673910-A 673 06-JAN-2004; Genome Therapeutics Corporation; Waltham, MA RES Location/Qualifiers 10.1410 /organism="unknown" /organism="unknown" /mol_type="genomic DNA"	AR450009.1 GI:42679066 Unknown. Unknown. Unclassified. 1 (bases 1 to 1410) Breton,G.L.	AR450009 Sequence 673 from pate AR450009	12617 ATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGATTGAC 12676 1321 CAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGACGATATTTTTTTGA 1380	7	1141 GGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGGC 1200	12377 TTTGGCATTTGAGCCTGTGATGGCGATGATTGGTGTGTTTGTT		CACCAAATCCATATTTGGATCGTTAATAATTCAAGTGCAGCGTGCCAATATTACCGCC 9	1219 1219 1229	721 GGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTTTCAAAAATACGCAATTTTTGTGC 780 	661 GATAATGGTGTGATTTGGGGCAACGCTTGTCAGTGTGGTCAAGCATTGCTTGGCTAAATT 720	
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901 CACCAPATCCATATTTTTGGATCGTTAATTAATTCAAGTGCAGGCGTGCCAATATTACCGCC 960	781 CAAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGCGGAGAGATTTAAAATTGT 840	732 GATAATGGTGTGATTTGGGGCAACGCTTGTCAGTGTGAAGCATTGCTTGGCTAAATT 673 721 GGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTTTCAAAATACGCAATTTTTGTGC 780	601 ATCACCATCATCAAATAAATAAAAATCTGCCGTTTGGTGGCTAAGCTAAGCTATTGTTGT 660	TTTGATTTTAATTGATGGATTGGTAAAAGTTTGTTTTTTT	972 Tracadcarraccorracadacarracarracarracarra	361 GCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATCAATATA 420	CAATGCCAGTGATGATATGCCATAAACCGTGCCAAGCCCATCAATTGCTGCAATGGTTGA	241 CTGCATAACCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA 240 1212 GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA 1153 241 CTGCATAACATATGCTGACAGCTCACTAAAATCTTGACCTTTACCAAGCCCACCCA	CATGCTAGCACAAGCAGGCGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA TACTGCCGATCAAGTGTACCAACCTGATATATTTTTAGATGCCAAATGTGGCATCACCTTT	1392 TAJAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTAAATTGATC 1333 61 CATGCTAGCAACAAGCAGGTGACAAAAGCACCCTAGCCGTGACTTTTGACTTGGCTGCCAA 120	Best Local Similarity 99.6%; Pred. No. 0; Matches 1374; Conservative 0; Mismatches 6; Indels 0; Gaps 0; Y 1 TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTAAATTGATC 60	99.38;

Query Match Best Local Similarity 53.5%; Pred. No. 7.1e-54; Matches 745; Conservative 0; Mismatches 572; Indels 75; Gaps 6; Qy 8 TGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTGATCCATGCTA 67	CP000082_20 2000001 2110000 CP000082_21 2100001 2210000 CP000082_22 2200001 2310000 CP000082_23 2300001 2410000 CP000082_24 2400001 2510000 CP000082_25 2400001 2510000 CP000082_26 2500001 2610000 CP000082_26 2600001 2650701 CP0010082_26 2600001 2650701 COntinuation 726 of 27) of CP0000082 from base 2500001 (CP000082 Psychrobacter arcticum 2		500001 600001 700001 800001 900001 1100001	ENT 2 5 8 2 2 5 8 2 2 5 8 2 2 5 8 2 2 5 8 2 8 2	b BESULT 4	1261 ATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGATTGAC	GAGCTTA	1081 TGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTTGAGCTTTT	Qy 1021 TTTGGCATTTGAGCCTGTGATGGCGATGATTGGTGTGTTTGTT
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Query Match Best Local Similarity 52.9%; Pred. No. 7.2e-48; Matches 726; Conservative 0; Mismatches 580; Indels 66; Gaps 7; Qy 5 GCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTAAATTGATCCATG 64	CR543861 14 1400001 1510000 CR543861 15 1500001 1610000 CR543861 16 1600001 1710000 CR543861 17 1700001 1810000 CR543861 19 1900001 2010000 CR543861 20 2000001 2110000 CR543861 21 2100000 22100000 CR543861 22 2200001 2310000 CR543861 23 2300001 25100000 CR543861 23 2300001 2510000 CR543861 25 2500001 2510000 CR543861 26 2600001 2710000 CR543861 27 2700001 2810000 CR543861 28 2800001 2710000 CR543861 29 2800001 3010000 CR543861 29 2800001 3010000 CR543861 30 300001 3110000 CR543861 31 3100001 310000 CR543861 33 3300001 310000 CR543861 33 3300001 310000 CR543861 33 3300001 3510000 CR543861 33 3300001 3510000 CR543861 35 3500001 3500001 CR543861 36 Of CR543861 from base 200001 (CR543861 Acinetobacter sp. ADP1 com	into 36 fragments Begin Er 100001 21 200001 31 300001 61 600001 61 600001 91 900001 91 1100001 111 1100001 131 1300001 131	!
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Breton,G. and Bush,D.
Nucleic acid and amino acid sequences relating
baumannii for diagnostics and therapeutics
Patent: US 6562958-A 1282 13-MAY-2003;
Genome Therapeutics Corporation; Waltham, MA
Location/Qualifiers
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AAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTAAATTGATCC

Conservative

0

Score 226.2; DB 6 Pred. No. 8.6e-44; 0; Mismatches 593

6

Indels Length

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Gaps

61

16.4**%;** 52.1**%**;

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TCTCGTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGA
                                                                                              CCGCCGACACCAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACA
                                                    CCGCCTACTGCAACTTTCTTACCTGCATCCTTAGCCATTAAGCCAATTAAAGTGGTTACA
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                                  GTACTTTTTGCATTGGAACCTGTAATCGCCACAATCGGCACATCAGTGGC------
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Sequence
AX932204
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Awrey,D., Beattie,B., Mansoury,K., Ouyang,H., Vallee,F.,
Richards,D., Nethery,K., Virag,C., Buzadzija,K., Pinder,B.,
Alam,M.Z., Tai,M., Canadien,V. and Kanagarajah,D.
Patent: WO 03087353-A 157 23-CCT-2003;
Affinium Pharmaceuticals, Inc. (CA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae
Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus.
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GCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATCAATATA
                                              CAAATGCAATTTACCCTCAATATA-----AAGCCCAGCCAATGCAGCAACTGTACT
                                                                          CAATGCCAGTGATGATATGCCATAAACCGTGCCAAGCCCATCAATTGCTGCAATGGTTGA
                                                                                                                                               TTGATTAATTAATTCAGCTAATTCTGAAAAATCAGCCCCTTTTCCGTCTCCGCCTAGCAA
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/mol_type="unassigned DNA"
/db_xref="taxon:727"
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Whole-genome random sequencing and assembly of Haemophilus
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The H. influenzae sequence has been updated by R. Fleischmann. New
database matches have been assigned, product names have been
improved, and a number of frame shifts have been corrected. We
gratefully acknowledge the work of Tatusov et. al. We have
incorporated their annotation into the /notes fields of the
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White,O., Clayton,R.A.,
Direct Submission
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Submitted (25-JUL-1995) The Institute
Medical Center Dr, Rockville, MD 20850
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The whole genome was shifted by 588 nucleotides
On Oct 1, 1996 this sequence version replaced gi
Location/Qualifiers
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Submitted (28-MAY-1998) The Institute for Genomic
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617. . 1582
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Dodson, R. and Gwinn,
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RLVGKNGSRTVRKDKRGNIVAHISDEKKYDAQDVTLSIDEKLGMYFREIKKAVSENN
AESGTAVLVDVRTGEVLAMATAPSYNPNNVGVKSELMKALSTNEDVSRLALRMP
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                      /note="similar to GB:D10483
GB:S49875 percent identity:
similarity; putative"
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3763. .5229
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ILLDLGVSSPQLDEAERGFSFNKDGPLDMRMOTTQGLSAEEWLKQVSIEDLTWYLKTF
GEBERFAKRIATAIUDENKSAVKNGTEFLSRTSGLAELISQAVDFKDKHGHATTSSGA
IRIFINSELDELESLLNSALDMLAPEGRLSIISFHSLEDRMVKHFMKKQSKGEDIPKG
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/note="similar to GB:D10483 SP:P18595 GB:X52063 PID:216497
PID:40850 percent identity: 62.09; identified by sequence
    AAAKKRLFTELDTQIKVINADDEIGYQWLTELPDAIAVSMNADFKVGSHQWMKAINIH
                                                                                                                                                                                                                                                            similarity; putative"
                                                                                                                                                                                                                                                                                PID:581032 percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSENNKPRYPLQQILVEDLFSSNKLVVLLLIGILVSAMGTIWIT
HKTRQLISENGMLILQRQALENEYRNLQVQEATEGDSTRVESIAISTLKMKVVSSEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity; putative"
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617. .1582
                                                                                                                    /protein_id="AAC22788.1"
/db_xref="GI:1574688"
                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                  /note="similar to GB:D10483 SP:P22188
PID:581032 percent identity: 55.72; id
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/protein_id="AAC22786.1"
/db_xref="GI:1574686"
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/protein_id="AAC22785.1"
/db_xref="GI:1574685"
                                                                                                                                                                                                                                                                                                                                      'gene="HI1133"
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/transl_table=11
                                                                                                                                                                                         product="UDP-N-acetylmuramyl-tripeptide
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53.11; identified by sequence
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Best Local Similarity
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8960 CGATGAAAATTTTGCAAGCAGCGCACCATCTCGACCAAAACAATAACAAATAATGTGTGG
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GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA
                                                                                                                                                                           TGTTGGGCGTAAAATTCTATCGCTTGTTCCATTGTATCGAACAA----ATAACTTTG
                                                                                                                                                                                                                                   TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTT
                                                                                                                                                                                                                                                                                                                                                         CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                  TAAACATTGAGCTAAATGCGTAAATTCTTCGCCGCGCTTTTCAAAAGAAGCAAACTGATC
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/protein id="AAC22789.1"
/protein id="AAC22789.1"
/db_xref="GI:1574689"
/translation="MIKISTYQLAQILQAKLIGDENVQVEKINTDTRKSVSNSLFFAL
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RTVAWTGSSGKTTVKEWTASILQHTAADSBAVLFTWANFANDIGVPLTLLRLTEKHRE
AVIELGANHQNEINYTKLVQPNAALINNIAPAHLBGFGSLAGVVQAKGEIYRGLTKN
GVAIINAEHNHLDIWQTEISNHAIQVFNGKOYSAKWIHHTSQGSTFTLISPQGEIEIT
LPYLGEHNVKNALAATALAMNVGATLTDVKAGLEQRSQVKGRLFPIQVTDNLLLLDDT
YNANKDSLCAALDVLKGYDAFRILCYGDMKELGENSLAIHHEVGQYINLVNLDLVCSY
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| TRALQILKFGQEVRNDGPESHFAKKGTPTMGGVMILFSIGVSTLWANLANPYINVCL
| FYLFGYGAIGFYDDFKKITRKNTDGLILARWKYFMMSVVALVAILWLYMLGHDTDATKI
| VIPFFKDIMPQLGLFYIVLSYFVIVGTGNAVNLTDGLDGLAIMPTALVAGAFALIAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="phospho-N-acetylmuramoyl-pentapeptide-
transferase E (mray)"
/protein_id="AAC22790.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="HI1135"
/gene="similar to GB:D10483 SP:P15876 GB:X51584 PID:216501
/note="similar to GB:D10483 SP:P15876 GB:X51584 PID:216501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="HI1134"
5243. .6616
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VCGRMEMIQYPNKPTVIVDYAHTPDALEKALIAAREHCQGELWCIFGCGGDRDRGKRP
LMAQVAEQFAEKIIVTKDNPRTESQSQIETDIVAGFKNMEKVGIIPDRAQAIQFAIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HI1136"
/note="similar to GB:D10483 SP:P14900 SP:P20100 GB:M30807
GB:X17609 percent identity: 60.96; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BPRVIIRFWIISLMLVLMGLVTLKLR"
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LGVVAILVRQEFLLVIMGGVFVVEALSVILQVGSYKLRKQRIFRMAPIHHHFELKGWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="HI1135"
6610. .7692
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/codon_start=1
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PID:42048 percent identity: 51.88; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="HI1136"
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49.6%;
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Pred. No. 5.6e-28;
0; Mismatches 606
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CCAAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGACGACGATATTTTTT
                                                                                                                                                                                                   GTGCGGTTTGAATTTCTGGTGTTTTTACCGCAAGCCCTGGGCTAATAACAATCATATCGC
                                                        TATCAATACCAGTAGGATTTTTTCGAGTATCAATCACACGAATATTAGCCTGTTGGGATA
                                                                                          TATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGATTGA 1319
                                                                                                                               TTTCAAGTAACCATTCCTGATTTAAACTACCAGTATGAAGAGGGATATTTTGAGGAAGTT
                                                                                                                                                                 CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGCAGTT
                                                                                                                                                                                                                                         TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGGCGTGCCAATATTACCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATCAATATA
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                                                                                                                                                                                                                                                                                                                                                  TTTTACCATTTGAACCTGTAATCCCCACAATTGGCTTTGTCGCTGCGCGCA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGCTGCCGCAGCTTTTAAGCTATAAGTTGTCTCAAGCTGAAAACTAGAAAGCTCTAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCTTGATTTTCGTTTTCCCCCAAAAGTCAGCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGATAATGGTGTGATTTGGGGCAACGCTTGTCAGTGTGGTCAAGCATTGCTTGGCTAAAT
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Pasteurellaceae; Haemophilus.
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Best Local Similarity 49.6%;
Matches 683; Conservative
CGACACCAACCAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACAGTGC
                                                                      CATAAAGTTCACAATCTTCATTC---AACAATGACAAAGCGGGAATCCCCAATATTTCCGC
                                                                                                        CCACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGGCGTGCCAATATTTACCGC
                                                                                                                                                                CCAAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGCGGAGAGATTTAAAATTG
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Pred. No. 4.2e-28;
0; Mismatches 606;
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	QY 181 GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA 240	OY 121 TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTT 180	Qy 61 CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA 120	QY 1 TAAAGCGTGAACCATGTTAACAACTTATCACCTCGCTCATTATAATTTTAAATTGATC 60	11.6%; Score 160.4; DB 6; Length 110000; nilarity 49.6%; Pred. No. 4.2e-28; Conservative 0; Mismatches 606; Indels 89; Gaps 7;	D426631 16 1600001 17 D426631 17 1700001 18 D426631 18 1800001 18 D426631 18 1800001 18	D426631 12 1200001 D426631 13 1300001 D426631 14 1400001 D426631 15 1500001	D426631 08 800001 91 D426631 09 900001 101 D426631 10 1000001 111 D426631 11 1100001 121	B 7 6 5	D426631_00 1 11 D426631_01 100001 21 D426631_02 200001 31 D426631_03 300001 41	426631_12/c COMMENT Sequence spl Fragment	g 8	1320 CCA	A 1319	Db 103327 TTTCAAGTAACCATTCCTGATTTAAACTACCAGTATGAAGAGGGATATTTTGAGGAAGTT 103268	103387 GTGCGGTTTGAATTTCTGGTGTTTTTTACCGCAAGCCCTGGGCTAATAACAATCATATCGC 103	1140 TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGG 1199	QY 1080 GTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTT 1139	103480 TTTTACCATTTGAACCTGTAATCCCCACAATTGGCTTTGTCGCTGCGCGGCA 103	Db 103540 CCATACCAACTTTCACACCAGCAGCTTTCGCCATTTCATAAACTAAAGTAGTTACGGTAC 103481 Oy 1020 TTTTGGCATTTGAGCCTGTGATGGCGATGATTGGTTTGTTT
Ş	Db Qy	당 \$	S B 8	, B &	da da	g dy	Qy db	Qγ	Db Qy	Qу	Qy	D Qy	р х	₽ Db	Qy D	; 8	문 \$	Ş B	\$ £	g 8
1320 CCAAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGGCATATTTTTT 1377	1260 TATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGATTGA 1319	3327 TTTCAAGTAACCATTCCTGATTTAAACTACCAGTATGAAGAGGGATATTTTGAGGAAGTT 3268	1140 TOGCOGCUACAMIACICOGOGITCTIGGGITAANGCCCGGGGCTGANGANGANCIGANCGGA 1199	1080 GTGCTTTGAGTGTATCAATGAACAATGCCTGATCACGAGGAATGCCTTGAGCTT 1139 3428	1020 TTTTGGCATTTGAGCCTGTGATGGCGATGATTGGTGTGTTTGTT	960 CGACACCAACAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACAGTGC 1019	900 CCACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGGCGTGCCAATATTACCGC 959	840 TIGCCCCTIGAGCIGCCAAAITIGAGAIAIGCTCAAGCIGAAAACITGACAGCTCAAGCA 899	780 CCAAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGCGGAGAGATTTAAAATTG 839	720 TGGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTTTCAAAAATACGCAATTTTTGTG 779	660 TGATAATGGTGTGATTTGGGGCAACGCTTGTCAGTGTGGTCAAGCATTGCTTAGCTAAAT 719	601 ATCACCATCATAATAAATAAAAATCTGC-CGTTTGGTGGCTAAGTAAGCTATTTGTTG 659	3926 AACCAATGTAGCTTCATCACAAGGTAAAATCACTTCATCATCTTTACCATTAAAATATTGCTT 3867		4046 TIGAAAACGATGATCTAACCCTTIGAAATGACGAAGTGCGGTACGAATTGAATCTAAATT 3987 481 AAGATIGGCAGCIGTGCCTAAGGCAAGIGCAGATAAGGCATTGAGTAAGGTTATGCTTGCC 540	421 TTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGGGTATCAAGCATGGCATGCAT	4106 CCCCACATTTGCTTTAGAGTCATTAATCCAACGAATGCCATTAGCTTGATGCACTAA 4047	4157 CARATGCARTTTACCCTCAATATAAAGCCCAGCCAATGCAGCAACTGTACT 4107	301 CAATGCCAGTGATGATATGCCATAAACCGTGCCAAGCCCATCAATTGCTGCAATGGTTGA 360	241 CTGCATAACATATGCTGACAGCTCACTAAAATCTTGACCTTTACCAAGCCCACCCA

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Fragment Name
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                                                                                                                                          TTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGGGTATCAAGCATGGCATCCATGGG
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                                                             AATACCTATAGCTTGTGCCAATGCTGTTGCTGCCAAAATGTTCATATAATTATGGCGACC
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Pred. No. 4.2e-28;
0; Mismatches 606;
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                                                                                                                                                                           Score 160.4; DB 6;
Pred. No. 4.2e-28;
0; Mismatches 606;
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1319	1260 TATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGATTGA
1259 103268	1200 CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGCAGTT
1199 103328	1140 TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCGG
1139 103388	1080 GTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTT
1079 103429	1020 TITTGGCATTTGAGCCTGTGATGGCGATGATTGGTGTGTTTGTT
1019 103481	960 CGACACCAACATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACAGTGC
959 103541	900 CCACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGGCGTGCCAATATTACCGC
899 103598	840 TIGCCCCTIGAGCIGCCAAAITIGAGATATGCTCAAGCIGAAAACTIGACAGCICAAGCA
839 103658	780 CCAAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGCGGAGAGATTTAAAATTG
779 103718	720 TGGCATCGTCTTGGTAGATGATGGCGGTTTTGGCAATTTTTCAAAAATACGCAATTTTTTGTG
719 103775	660 TGATAATGGTGTGATTTGGGGCAACGCTTGTCAGTGTGGTCAAGCATTGCTTGGCTAAAT
659 103807	601 ATCACCATCATCAACAAATAAAATCTGC-CGTTTGGTGGCTAAGTAAGCTATTTGTTG
600 103867	541 TTIGATTITAATIGATGGATTIGGTAAAAGTTTGTTTTTTTGATGATATAATGCCATACC
540 103927	481 AAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAGGTTATGCTTGCC
480 103987	421 TTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGGGTATCAAGCATGGCATCCATGGG
420 104047	361 GCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATCAATATA
360 104107	301 CAATGCCAGTGATGATATGCCATAAACCGTGCCAAGCCCATCAATTGCTGCAATGGTTGA
300 104158	241 CTGCATAACATATGCTGACAGCTCACTAAAATCTTGACCTTTACCAAGCCCACCCA
240 104218	181 GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA

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103207	1320	103267
103207 AGAGATAATCCACACAAGAAAGACCTGTTTTGCCAAGCCCGATGATAGTAATATTTTT 103150	1320 CCAAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGGCATATTTTTT 1377	

Search completed: May 12, 2006, 09:55:03 Job time: 7232 secs

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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1 taaagcgtgaaccatgttaa.....acgacggcatatttttttga 1380
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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#	44.4	44.4	44.4	45	45	45	46	47.2	47.6	49.4	49.8	50.2	52.6	55	56.8	62.2	69.8	77.2	92	92.8	98.2	Score	
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2.9	2.9	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3. 0	3.0	3.0	3.1	3.1	3.1	3.1	3.1
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ALIGNMENTS

	FEATURES source		JOURNAL COMMENT	TITLE	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 CZ543630/C LOCUS DEFINITION ACCESSION
/organism="Strongyloldes ratti" /mol_type="genomic DNA" /strain="Isofemale line ED321 heterogonic" /db_xref="taxon:34506" /db_xref="taxon:34506" /dev_stage="infective larval stage (iL3)" /lab_host="GS10" /clone_lib="strongyloides ratti whole genome shotgun /clone_lib="strongyloides ratti whole genome shotgun library (gRAAGSS 004)" /note="Vector: pOTW13; Site_1: BstX1; Site_2: BstX1; Strongyloides ratti genomic DNA was randomly sheared, end-repaired and size fractioned to enrich for 2-4 kb end-repaired and size fractioned to enrich for 2-4 kb fragments. Genomic DNA was provided by Fiona Thompson		Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: nematode@watson.wustl.edu Genomic DNA was provided by Fiona Thompson (F.Thompson@bristol.ac.uk) and Mark Viney (Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol,	•	Ritter, E., Martin, J., Wylie, T., Dante, M., Waterston, R.H., Clifton, S.W. and Wilson, R. Genome Survey sequences from the rat parasitic nematode	<pre>Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Panagrolaimoidea; Strongyloididae; Strongyloides. 1 (bases 1 to 817) Mitreva,M., McCarter,J.P., Thompson,F., Viney,M., Pape,D.,</pre>	CZ543630.1 GI:64673383 GSS. Strongyloides ratti Strongyloides ratti	CZ543630 817 bp DNA linear GSS 13-MAY-2005 SRAA-aad51b03.g1 Strongyloides ratti whole genome shotgun library (SRAAGSS 004) Strongyloides ratti genomic, genomic survey sequence.

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 709)
Kim, J. S., Jun, K.M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, 1
Song, S. I., Kim, J. K., Kim, Y. - K. and Nahm, B. H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             709 pp mRNA linear EST 15-AUG-2003 HDA1--05-E12.g1 OsHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDA1) Oryza sativa (japonica cultivar-group) cDNA clone HDA1--05-E12, mRNA sequence.
CF306440
                                                                                                                                                                                                                                                                                             Genomics and Genetics Institute, of Bioscience and Bioinformatics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF306940
CF306940.1 GI:33678701
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82 31 330 6193
82 31 321 6355
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Location/Qualifiers
     /db_xref="taxon:39947"
/clone="HDA1--05-E12"
/tissue_type="callus"
/dev_stage="proliferated callus on 21
/lab_host="E.coli SOLR"
/clone_lib="0sHDAC1-overexpressing typhage CDNA library I (HDA1)"
/clone___
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                                                                                                                               organism="Oryza sativa
/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 1.3e-16;
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                                                                                                                                                                                                                         bhnahm@bio.myongji.ac
                                                                                                                                                                                                                                                                                               GreenGene Biotech II
, MyongJi University
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Matches
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                                                                                                                                                                         Genome Center
University of Washington
Box 352145, Seattle, WA 98
Tel: 2062216954
Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      958 GCCGACACCAACAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            msh2_
                                                                                                                                                                                                                                                                             Whole-Genome-Sequence variation Psedomonas aeruginosa library J. Bacteriol (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                               Contact: Chris K.
                                                                                                                                                                                                                                                                                                                            Spencer, D.H., Raymond, C.K., Smith, Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic survey sequence BZ579116
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BZ579116.1
                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _6205.y2 msh Pseudomonas
                                                                                                                                                 shotgun.
                                                                                                                                                             craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescript SK(+); Site 1: EcoRI; S: XhOI; Callus was treated with ABA(20um) for lhour. was inserted into lambda Uni-ZAP XR vector at 5' en EcoRI and 3' end with XhoI site. mENA was derived rice Histone Deacetylase overexpression line."
                  /clone_lib="msh"
                              /db_xref="taxon:287"
/clone="msh2_6205"
                                                                /mol_type="genomic
/strain="MSH"
'note="Environmental isolate. Whole genomic shotgun
                                                                                                organism="Pseudomonas
                                                                                                                                ocation/Qualifiers
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Pred. No. 4.4e
0; Mismatches
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No. 4.4e-15;
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Matches 192;
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                                                                                  This work and Genetic Resource Center Saga Ippongi-cho, Ukyo-ku, Saga Ippongi-cho, Ukyo-ku, 8:-1. a1-75-873-2660 FAX: 8:
                                                                                                                                                                                                                                                 Submitted (19-JAN-2005) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170
Clones are derived from the BAC library DNB1
For BAC library availability, please contact Masa-Toshi Yamamoto
                                 Sequencing : LIBRARY
                                                                                                                                                     (Yamamoto@kit.jp).
Submitted (30-11-2004) by Masahira Hattori,
RIKEN, Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa
(E-mail:hattori@gsc.riken.jp, Tel:81-45-503-9111,
Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
AG943479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila ananassae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS
                                                                                                                                     This work was done in collaboration with Yamamoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                               BAC end sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hattori,M., Toyoda,A., Murakami,K., Toshio,T.K. and Sakaki,Y.
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nilarity 56.3%;
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                        Vector
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Sacl
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Pred. No. 8e-15;
0; Mismatches 146; Indels
                                                                                        1, Kyoto 616-8354,
81-75-861-0881
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                                                                                                                                                                                       230-0045,
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pacs2-164_8171, genomic survey semieron
                                                                                                                                                                                                                                                                   1 (bases 1 to 1445)
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E.,
Burns,J.L., Kaul,R. and Olsen,M.V.
Whole-Genome-Sequence variation among multiple isol
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                   University of Washington
Box 352145, Seattle, WA
                                                                                                                                                                                                                                      Genome Center
                                                                                                                                    Class: shotgun.
                                                                                                                                                                                                                                                      Contact: Chris K.
                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BZ568959.1 GI:27202799
                                                                                                                                                  Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa
                                                                                                                                                                       2066857244
                                                                                                                                                                                       2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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/db_xref="taxon:287"
/clone="pacs2-164_8171"
/clone__lib="pacs2-164"
                                                 /mol_type="genomic DNA"
/strain="2-164"
                                                                                                                  Location/Qualifiers
                                                                                 organism="Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .555
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                                                                                                                                                                                                                                                      Raymond
                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas
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                                                                                  aeruginosa"
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genomic clone

USA

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GTTAATAAAACGGTTGTTGTGGATTTCCCCATTTGTGCCTGTGATGGCAACAAAACGTGCT
                                                                                                                                                                                                                                            GCAGGCGTGCCAATATTACCGCCGACACCAACAATCATGCCTGCATGTTTTGCCATCTCG 997
                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAAAACTTGACAGCTCAAGCACCACCAAATCCATATTTTGGATCGTTAATAATTCAAGT
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                                                                                                                                                                                                                                                                                                         GCAGCAGGACCTAAATTCCCTCCTGCCATCGCAGGAATACCAGCTTCATTTAAAAGATGT 187
                                                                                                                                                                                                                                                                                                                                                                                                       ATATAAGAGGACATCTCTAGAACATATACGCCTTGATCATCCAATAAAGGAAGAGCCAGT
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/mol_type="genomic DNA"
/db xref="taxon:721"
/clone="DNB1-017M23.R.fa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_lib="DNB1 Drosophila"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 77.2; DB 10;
Pred. No. 1.4e-10;
0; Mismatches 143;
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ORGANISM
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AG952088
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                        Sequencing LIBRARY
                                                                                                             Genetic Resource Center
Saga Ippongi-cho, Ukyo-ku, Kyoto 616-8354,
Tel: 81-75-873-2660 FAX: 81-75-861-0881
                                                                                                                                                                                     (yamamoto@kit.jp).
Submitted (30-11-2004) by Masahira Hattori,
RIKEN, Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa
(E-mail:hattori@gsc.riken.jp, Tel:81-45-503-9111,
Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                         Submitted (19-JAN-2005) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mall:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the BAC library DSE1

Clones are derived from the BAC library DSE1

Clones are derived from the BAC library DSE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
AG952088
AG952088.1 GI:58473786
GSS
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BAC end sequences of Library DNB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila sechellia
Drosophila sechellia
                                                                                                                                                                    This work was done in collaboration with Yamamoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila sechellia DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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       R.Site
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                                         Vector
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library."
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55.0%;
   : pKS150
: Sacl
: Sacl.
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Pred. No. 2.5e-08;
0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    623 bp DNA linear clone: DSE1-004A05.F.fa,
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genomic survey
                                                                                                                                                                                                                         230-0045,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1003
                                                                                                                          Evolutionary Biology
Max-Planck-Institute for Developmental Bi
Spemannstr. 37-39, Tuebingen D-72076, Ger
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pa
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           883 ACTTGACAGCTCAAGCACCAACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 823 GGAGAGATTTAAAATTGTTGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             763 AATACGCAATTTTTGTGCCAAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                703 GCATTGCTTGGCTAAATTGGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTTTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CL691264 628 bp DNA PRIO156a AOS 2 - PRIO156a BR (628) Mixe pacificus var. California Pristionchus
                                                                                            Seq primer:
Class: fosm
                                                                                                                                                                                                                                                                                                              Pristionchus pacificus
Nucleic Acids Res. 32 (
                                                                                                                                                                                                                                                                                                                                                  Srinivasan, J., Otto, G.W., AppaDB: an AcedB database
                                                                                                                                                                                                                                                                                                                                                                                                   Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                            Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pristionchus pacificus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CL691264.1 GI:50213172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAATGTCGTAACAGTGCTTTTGGCATTTGAGCCTGTGATGGCGAT 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACGCCTAAATTTCCACCAATAGCTACTTTTTTCCCTGCAGATTTTAATATGTGCCCTAT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTGCCAATATTACCGCCGACACCAACAATCATGCCTGCATGTTTTTGCCATCTCGCCTAC 1002
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                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 628)
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                                                                                            fosmid ends
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
                                                                         Location/Qualifiers
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/db_xref="taxon:7238"
/clone="DSE1-004A05.F.fa"
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51.0%;
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Pred. No. 3.1e-
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Best Local :
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                       Department of Plant Pathology and National Taiwan University NO.1, Section 4, Roosevelt Road, TTel: 886 2 3366 4595
                                                                                         Analysis of expressed sequence tags from Antrodia cinnamomea, polypora causing brown rot of Cinnamomum kanehirai Unpublished (2005)
                                                                                                                                                                                                                                                                                bda020270D15.ab1_061 A
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                                                                              Contact: Tzean SS
                                                                                                                                       Shiao, M.S.
                                                                                                                                                                                             Eukaryota; Fungi; Basidiomycota;
                                                                                                                                                                                                            Antrodia cinnamomea
Antrodia cinnamomea
                                                                                                                                                                                                                                         EST.
                                                                                                                                                                                                                                                     DR032465.1 GI:66834715
                                                                                                                                                   Tzean, S.S., Hwang, S.T.,
                                                                                                                                                                                 Aphyllophorales; Antrodia.
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          886 2 3366 4595
886 2 2362 0639
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sst@ntu.edu.tw
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/clone_lib="Mixed stage fosmid library of
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
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                                     Taipei 10617,
                                                                                                                                                                                              Hymenomycetes;
                                                                Microbiology
                                                                                                                                                  Liou, R.F.,
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1171 bp DNA linear
pacs2-164 1863.x1 pacs2-164 Pseudomonas aeruginosa
pacs2-164 1863, genomic survey sequence.
                                                                                                                                                                                                                                                                                Whole-Genome-Sequence variation Psedomonas aeruginosa library J. Bacteriol. (2002) In press
                                                                                                                                                                                                    Box 352145, Seattle, Tel: 2062216954
                                                                                                                                                                                                          Genome Centre of Washington University of Washington 98105-2145,
                                                                                                                                                                                                                                                                    Contact: Chris K.
                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1171)
Spencer,D.H., Raymond,C.K., Smith,E.E.,
Burns,J.L., Kaul,R. and Olsen,M.V.
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
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: 5' CACACAGGAAACAGCTATGACCAT 3'
                                                                   /organism="Pseudomonas
/mol_type="genomic DNA'
/strain="2-164"
/db_xref="taxon:287"
/clone="pacs2-164 163"
/clone lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
                                                                                                                                    Location/Qualifiers
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/mol_type="mRNA"
/strain="SMV 1"
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/lab_host="Cinnamomum kanehirai"
/clone lib="Autrodia cinnamomea cDNA
/note="Vector: ZAP Express Vector"
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Pred. No. 0.00035;
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Best Local Similarity
Matches 170; Conserv
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                                                                                                                                                                                                                                                                                                                                             Washington University in St. Louis
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                 Email: nematode@watson.wustl.edu
Genomic DNA was provided by Fiona Thompson
(F.Thompson@bristol.ac.uk) and Mark Viney
(Mark.Viney@bristol.ac.uk) at the University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRAA-aad60c01.
(SRAAGSS 004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitreva, M., McCarter, J.P., Thompson, F., V. Ritter, E., Martin, J., Wylie, T., Dante, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Panagrolaimoidea; Strongyloididae; Strongyloides.
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CZ545153.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strongyloides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Survey sequences from the rat parasitic nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clifton, S.W. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATATTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGGGTATCAAGCATGGCATCCA 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGGCAGGCGGACCGCATGGCCAGCTCGGCGAGCGCGTTG
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                                                                                                                                                                                                                                 shotgun
                                                                                             /organism="Strongyloides ratti"
/mol_type="genomic DNA"
/strain="Isofemale line ED321 heterogonic"
/db_xref="teaxon:34506"
/dev_stage="infective larval stage (417)"
 /note="Vector: pOTW13; Site_1: BstX1; Site
Strongyloides ratti genomic_DNA was random
                                                                                                                                                                                                               Location/Qualifiers
                                     clone_lib="Strongyloides ratti whole genome shotgun
ibrary (SRAAGSS 004)"
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.gl Strongyloides ratti whole
Strongyloides ratti genomic,
                                                                           stage="infective larval stage (iL3)"
host="GS10"
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Pred. No. 0.0022;
0; Mismatches 174;
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ratti whole genome shotgun library
tti genomic, genomic survey sequence
DNA
                                                                                                                                                                                                                                                                                                                                                                                   Louis,
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                                                                                                                                                                                                                                                                                                                                                                                   63108,
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                   ا<sub>د</sub>.
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ACCESSION
VERSION
KEYWORDS
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           946 GCCAATATTACCGCCGACACCAACAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAA 1005
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                                                                                                                                                                                                                                                                                                    Sequenced from the Brugia malayi BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by The Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in collaboration with Mark Blaxter, ICAPB, University of Edinburgh, UK Seq primer: T7 (TAATACGACTCACTATAGGG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 GCCAATATTTCCGCCTAAACCAACATTCAATCCTTCATTTTTCAGGATGTGATAGATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Blaxter ML
Institute of Cell, Anima
University of Edinburgh
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Onchocercidae; Brugia.

Onchocercidae; Brugia.

Onchocercidae; Brugia.

Onchocercidae; Brugia.

Whitton,C., Daub,J., Quail,M., Hall,N., Foster,J.,
Whitton,C., Daub,J., Quail,M., Hall,N., Foster,J.,

Ganatra,M., Slatko,B., Barrell,B. and Blaxter,M.

A genome sequence survey of the filarial nematode
repeare, gene discovery, and comparative genomics
Mol. Biochem. Parasitol. 137 (2), 215-227 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH795426
BMBAC376G09T7_PSU Brugia malayi Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
Sequenced from the Brugia ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashworth Labs, King's Buildings, West Mains Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
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BH795426
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/(sex="Mixed (male and female)"
/tissue_type="whole parasite"
/dev_stage="microfilaria (L1)"
/clone_lib="Brugia malayi Genomic Bac Library 3"
/note="Vector: pBACe3.6; Site_1: BamH I; Brugia malayi
genomic DNA was partially code with Sau3A I and size
fractionated. 7,392 clones were generated with mean insert
size -48 kbp. The library was constructed by Claire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              end-repaired and size fractioned to enrich for 2-4 kb fragments. Genomic DNA was provided by Fiona Thompson (F.Thompsonobristol.ac.uk) and Mark Viney (Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol, UK. Sequencing by Washington University Genome Sequencing Center, St. Louis, MO."
                                                                                                                                                                                                     /organism="Brugia malayi"
/mol_type="genomic DNA"
/strain="TRS"
                                                                                                                                                                              db_xref="taxon:6279"
                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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Pred. No. 0.01
0; Mismatches
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3 Brugia malayi
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=PM4-HT0688-050
500-002-dl0&t3=2000-05-05&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 452)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                     Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simpson, A.J.
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PM4-HT0688-050500-002-d10
BE184674
BE184674.1 GI:8663858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                    quality sequence start: 26 quality sequence stop: 89. Location/Qualifiers
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/note=Torgan: head neck; Vector: puc18; Site 1: SmaI; /note=Torgan: head neck; Vector: puc18; Site 1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                   /organism="Homo sapiens'
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whitton, Blaxter Nematode Genetics Lab, University of Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing Unit, The Sanger Centre, Cambridge, UK."
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                                                                                                                                                              _stage="Adult"
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Pred. No. 0.01:
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Best Local Similarity
                                                                                                                                                                                                                Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                  and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fly), genomic survey sequence.
AL068607
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BACR32D23 of RPCI-98 library from
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                /mol_type="genomic DN
/db_xref="taxon:7227"
/clone="BACR32D23"
                                                                                                                               Location/Qualifiers
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clone_lib="RPCI-98"
                                                                                     organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 TTGCTATCAATATCATCAATATATTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGG 457
                                                                                                                                                                          Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphieme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL097862
AL097862.1 GI:5609473
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genome sur
BACN02P17 of DrosBAC library from
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                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                              pBeloBAC11.
                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TKDKKKKAWAAWNDTTDGKTKAKKADTKADTGKKGAKATKAAKAKGWDADADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGCGGAGAGATTTAAAATTGTTGCCCCTTGAGCTGCCAAATTTGAGATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAAAAATACGCAATTTTTGTGCCAAATAATCCACCATGCCATCGTGCCGATCAAGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCAAGCATTGCTTGGCTAAATTGGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGCTAAGTAAGCTATTTGTTGTGATAATGGTGTGATTTGGGGCAACGCTTGTCAGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTGTAWKTKTGKKKKKGKKKGKKGKDWTKGTKWDTKTKTKGKKTGSGGGKKKTKYKGTKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGKKKGRKWKKGGKGKKKTKDGTKKKKTTGKWDDDDAWWDWWADTDWKKAGGGGGKGKDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic survey sequence.
                                         /mol_type="y=.....7227"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
                                                                        organism="Drosophila melanogaster"
/mol_type="genomic DNA"
                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.4%;
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Pred. No. 0
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Burvey sequence SP6 end of BAC
rom Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy Spermatophyta; Coniferopsida, Coniferales; Pinaceae; Picea.

1 (bases 1 to 823)

Ralph, S., Kolosova, N., Oddy, C., Cooper, D., Butterfield, Y., Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, Mayo, M., Moran, J., Olson, T., Wong, D., Friedmann, M.F., Ritland, C. Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C. Ritland, K. and Bohlmann, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WS02715.BR P20 SS-IL-A-FL-14
WS02715 P20 3, mRNA sequence.
DR505933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Joerg Bohlmann Genome BC forest genomics program University of British Columbia Michael Smith Laboratories, 6174 University Boulevard, Vancouver, British Columbia, Canada, V6T 1Z3 Tel: 1-604-822-2114 Fax: 1-604-822-2114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bohlmann@msl.ubc.ca
Plate: WS02715 row: P co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Picea sitchensis (Sitka spruce)
Picea sitchensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop:
                      /db xref="taxon:332"
/clone="WS02715 P20"
/sex="Hermaphrodite"
/lab_host="E. coli DHIOB cells"
/clone lib="SS-IL-A-FL-14"
/clone lib="SS-IL-A-FL-14"
/note="Organ: Green portion of the leader tissue from year old clonal trees grown under greenhouse condition standard potting soil mixture; Vector: pBluescript II (+) XR; Site_1: XhoI (5' end of cDNA); Site_2: BamHI (end of cDNA); Site_3: BamHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="FB3-425"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Picea sitchensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="end : SP6"
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independently and equal quantities
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Pred. No. 0.
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Picea.
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Qy 62 ATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAAT	Qy 2 AAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATCC	Query Match 16.4%; Score 226.2; DB 3; Length 1416; Best Local Similarity 52.1%; Pred. No. 1.1e-58; Matches 718; Conservative 0; Mismatches 593; Indels 66; Gaps	; LENGTH: 1416 ; TYPE: DNA ; ORGANISM: Acinetobacter baumannii US-09-328-352-1282	SEZOO	O ACID SEQUENCES RELATING TO	OMOI	RESULT 3	Db 72 CAAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGGCATATTTTTTTGA	Oy 1321 CAAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGGCATATTTTTTTGA	Dy 1261 ATCTGCCAAGGTAGGATTGGATTCATCGATGATGTTTTTGTGACCGTGATTGAC	192	QY 1201 TGAGCTTAAGAGTTCACTGTCCAAAGCTGCCAAAATGAACAATGAACGCCTGTGGGCAGTT	Oy 1141 GGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATGATCGGC		UD 372 TITGGCATTTGAGCCTGTGATGAGAAGAATTGGTGTGTTTTGTTGAGATTAGATCTCG Qy 1081 TGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTTAAGCTTT	1021 TTTGGCATTTGAGC	961 GACACCAACAATCATGCCTGCATGTTTTGCCATCTGCCTACTAATGTCGTAACAGTGCT	492	Qy 901 CACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGGCGTGCCAATATTACCGCC	CY 841 TGCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCAC Db 552 TGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCAC Db 552 TGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCAC	612	Qy 781 CAAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGCGGAGAGATTTAAAATTGT	Qy 721 GGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTTTCAAAAATACGCAATTTTTGTGC
	2 61 Qy	Oy Db	D dy	D Qy	ACINETOBACTER Db	Oy do	Db	13 Oy	1380	C 1320 Db	r 133	1260	C 1200 Db	253	G 313 Qy		T 1020 Db	C 433 Qy	960	C 900 Db	T 553 Qy	840	C 780 Db
1136 GCTTTGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGA 1195	1076 TCTCGTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGA 1135	1016 GTGCTTTTGGCATTTGAGCCTGTGATGGCGATGATTGGTGTTTGTT	956 CCGCCGACACCAACAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACA 1015	896 AGCACCAACTCATATTTTGGATCGTTAATAATTCAAGTGCAGGCGTGCCAATATTA 955	836 ATTGTTGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCA 895	776 TGTGCCAAATAATCCACCATGCCATCGTGCCGAGATCAAGATGATCAGCGGAGAGATTTAAA 835	715ACGCATCATCTCGGTTAAATACAACTTTTTTAGCGCCTTGGAAAATACGATGTTTT 660	CGCAATTTT	TTAAACCAAAGCTTTGCATTGGTGTCTGGAACAAGTGGACGGCTTA	818 AGCGTACCGTCGGCATCTCTTÄAAACGCCATATTGATTTÄÄATCCGGTGCGT 767 656 GTTGTGATAATGGTGTGATTTGGGGCAACGCTTGTCAGTGTGGTGAAGCATTGCTTGGCT 715	596 ATACCATCACCATCAACAATAAATAAAAATCTGCCGTTTGGTGGCTAAGCTAAGTT 655		938 ATAGGTAAACCAATTGCTTCCCCCAATGCTAAACAAGCTAAAGCATTAGCTACATTGTGC 879 536 TTGCCTTTGATTTTAATTGATGGATGGTAAAAGTTTGTTT	476 ATGGAAGATTGGCAGCTGCTGCCTAAGGCAAGTGGAATAAGGATTAAGGTTATGC 535	416 ATATATTCACAGCGATGCGGTAGCCCCTTTGAAAGTCTTAAGGGTATCAAGCCATGGCATCC 475		1118 AGTGCAACCTTACCTTTTTTCACTTCAATGGCAGCACCTAAGCCATCAATTGCTGCAAGT 1059 356 GTTGAGCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATCA 415	302 AATGCCAGTGATGATATGCCATAAACCGTGCCAAGCCCATCAATTGCTGCAATG 355	1178 TTTTCGATAGAAGGAACGTAAAGGAGAAAAATCTTGTCCTTTGCCCTGTCCACCTAAAATA 1119	1238 TGAĀTGGCTTGTTCGĀTGĀCĀGGGGCĀTCTTCĀCCĀĀTCĀĀTĀCCĀCĀACTTTGGCĀTĀT 1179 242 TGCĀTĀĀCĀTĀTGCTGĀCĀGGTCĀCTĀĀĀĀTCTTGĀCCTTTĀCCAĀGCCCĀĀCĀCCCAĀĀĀTC 301	182 AGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCAC		1349 AAACTTGCACATGCTGGTGATAGCAATACCACATCTTCAGCTTGTGTTTCAC 1298 122 ACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTTG 181

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US-09-557-884-1/c
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Sequence 1, Application US/0955/00~
Sequence 1, Application US/0955/00~
PATENT NO. 6506581
; GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae
The Haemophilus influenzae
The Haemophilus influenzae
The Haemophilus influenzae
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APPLICATION NUMBER: 08/476,102

PILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEPHONE: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base paix8
                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                     Matches 683;
                                                                  1204379
                                                                                                                                                                                                                                                         Local
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MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
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TACTGCCCGATCAAGTGTACCAACCTGATATTTTAGATGCCAAATGTGCATCACCTTT
                                                                GAGACTTGCACAAGCAGGCGACAATAATACCA-----TATCTCCGCTTTGCAA
                                                                                                                                                                                        TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text
SUT APPLICATION NUMBER: US/09/557,884
PILIANG DATE: 25-Apr-2000
CLASSIFICATION: -Unknown>
                                                                                                                                                  TAAACATTGAGCTAAATGCGTAAATTCTTCGCCGCGCTTTTCAAAAGAAGCAAACTGATC
                                                                                                      CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA
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  TTTCAAGTAACCATTCCTGATTTAAACTACCAGTATGAAGAGGGATATTTTGAGGAAGTT
                                                                                    GTGCGGTTTGAATTTCTGGTGTTTTTACCGCAAGCCCTGGGCTAATAACAATCATATCGC 1203328
                                                                                                                            TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGG
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RESULT 5
US-09-643-990A-1/c
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
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                                                                                                                                                                              ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-643-990A-1
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                                                                                                                      Query Match
Best Local Similarity
Matches 683; Conserv
                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
                  1204379
                                                                      1204439
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: 9B186P10
TELEPHONE: 301-610-5990
TELEPHONE: 301-610-5990
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION INVBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
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CORRESPONDENCE ADDRESS: 1
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
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                                                                                    TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC
                GAGACTTGCACAAGCAGGCGACAATAATACCA---
                                        CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA 120
                                                                                                                                                                                                        STRANDEDNESS: double TOPOLOGY: linear
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Owen White
Hamilton O. Smith
J. Craig Venter
OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd
Thereof, and Uses Thereof
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Pred. No. 9.2
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1203926 AACCAATGTAGCTTCTTCACAAGGTAAAATCACTTCATCTTTTACCATTAAATATTGCTT 1203867
1200 CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGCAGTT 1259
                                                                                     GTGCGGTTTGAATTTCTGGTGTTTTTACCGCAAGCCCTGGGCTAATAACAATCATATCGC 1203328
                                                                                                                                                        TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATGATCATCGG
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SEQ ID NO 1
LENGTH: 1830121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Patent No. 6846651
TITLE OF INVENTION: Thereof, and Uses Thereof
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APPLICANT: Fleischmann et al.
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CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 09/557,884
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
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                     NAME/KEY: misc feature
LOCATION: (44416)..(44416)
OTHER INFORMATION: n equals
                                                                                             NAME/KEY: misc_feature
LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals
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LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a,t,c,
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NAME/KEY: misc_feature
LOCATION: (36551)...(36551)
OTHER INFORMATION: n equals
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals
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LOCATION: (4747)...(4747)
OTHER INFORMATION: n equals
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LOCATION: (9921)..(992
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LOCATION: (36543)..(36543)
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LOCATION: (51786)..(51
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LOCATION: (51602)..(51
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NAME/KEY: misc_feature
LOCATION: (117136)..(117136)
OTHER_INFORMATION: n equals
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals
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LOCATION: (105121)...(105121)
OTHER INFORMATION: n equals
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals
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LOCATION: (100091)..(100091)
OTHER INFORMATION: n equals
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LOCATION: (65313). (65313)
OTHER INFORMATION: n equal
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LOCATION: (65309)...(65309)
OTHER INFORMATION: n equal
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LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals
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LOCATION: (44905)...(44905)
OTHER INFORMATION: n equals
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LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals
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LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals
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LOCATION: (45593)..(45593)
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LOCATION: (44975)...(44975)
OTHER INFORMATION: n equals
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals
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LOCATION: (47036)..(47036)
OTHER_INFORMATION: n equals
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LOCATION: (45732)..(45732)
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OTHER INFORMATION: n equals
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Query Match
Best Local Similarity
Matches 683; Conserv
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OTHER INFORMATION: n equals a,t,c, or
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NAME/KEY: misc_feature
LOCATION: (119924)...(119924)
OTHER INFORMATION: n equals a,t,c, or
FEATURE:
NAME/KEY: misc_feature
LOCATION: (120038)...(120038)
OTHER INFORMATION: n equals a,t,c, or
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NAME/KEY: misc_feature
LOCATION: (140398) .. (140398)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (142750) .. (142750)
OTHER INFORMATION: n equals a,
                                                      PEATURE:
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals
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NAME/KEY: misc feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals
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LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals
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LOCATION: (145171)...(145171)
OTHER_INFORMATION: n equals
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a,t,c,
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NAME/KEY: misc_feature
LOCATION: (131360)..(131360)
OTHER_INFORMATION: n equals a,t,c,
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LOCATION: (145942)...(145942)
OTHER INFORMATION: n equals
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LOCATION: (139910)...(139910)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (122167)...(122167)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals a,t,
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US-09-543-681A-2830/c
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Best Local S
Matches 352
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APPLICANT: GARY HERTON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2830
LENGTH: 1323
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Proteus mirabilis
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    1140 TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGG
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                                                                                     GTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTT
                                                                                                                                                               CGACACCGACAGGGATCCCGTCAGCTTTAGCCATTTCCCCCCACCAACGTCGTTACGGTAC
                                                                                                                                                                                                                                                                                                      CATATAAGTCATAAGGCTGT---GTTAATAACGTTAAAGCAGGTACACCAATATTGCCAC
                                                                                                                                                                                                                                                                                                                                               CCACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGGCGTGCCAATATTACCGC
                                                                                                                                                                                                                                                                                                                                                                                          TGGCAGCCGCCGCTGTTAAGCTATAGGTTGTCTCTAATTGAAAGCTCGATAGCTCTAAGA
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                                                                                                                                TTTTGCCATTAGAGCCTGTTATCGCAACAATAGGTGCTTTTGCCTCACGG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGCAGTT 1259
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US-09-252-991A-7702/c
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Best Local Sim:
Matches 506;
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SEQ ID NO 7702
LENGTH: 1371
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                  1238 ACTGCTTCGTCCAGCGTTGCGACGCGCACCAGCGGTACCGCGTTGCCCAGTGCCTGGGCA
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AGGCCGGAAAAACGCCTTCAGCGCGCGAGCATGGCGTCGAACGGCAGGCCGACCGCATGG
                                        AGCCCTTTGAAAGTCTTAAGGGTATCAAGCATGGCATCCATGGGAAGATTGGCAGCTGTG
                                                                                   TTGGAATCGTCGTAGTAGCTCACGCCCTGCCGCTCGCGTACCCACTGGCAGCGATGAGCC
                                                                                                                           TTTGAATCATTAAAATATGCCTTGCTATCAATATCATCAATATATTCACAGCGATGCGGT
                                                                                                                                                                                                            ATGCCATAAACCGTGCCAAGCCCATCAATTGCTGCAATGGTTGAGCCGATGTTTGTACCT
                                                                                                                                                                                                                                                            CGCAGGTCATGGAAATCGGCGCCCTTGCCGTCTCCGCCGGCGAGCAGCACCAGCTTGCCG
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Pred. No. 3.5e-25;
0; Mismatches 500
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Gaps

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196

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136

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Sequence 7861, Application US/09252991A

Retent No. 651795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SE

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND

FILE REFERENCE: 107196, 136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-07-27

NUMBER: OF SEQ ID NOS: 33142

SEQ ID NO 7861

LENGTH: 1401

TYPE: DNA

ORGANISM: Peeudomonas aeruginosa

US-09-252-991A-7861
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US-09-252-991A-7861
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                                                                                                       Query Match
Best Local Similarity
Matches 506; Conserv
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      GGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAATACTGCCCGATCAAGT
                                                                   TTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATCCATGCTAGCACAAGCA
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                                    TTGGCGAACAGGCGTCCGCGTTCTTCGAAGTTCTTGAACATGTCCAGGCTCGCGCAGGCC
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CURRENT APPLICATION NUMBER: US/09/701,229
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/087,308
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: PCT/US99/11585
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
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Best Local Sim
Matches 506;
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APPLICANT: Azzolina, Barbara
TITLE OF INVENTION: MUED PROTEIN A
TITLE OF INVENTION: AERUGINOSA
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ORGANISM: Pseudomonas
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                                                                                         GGGGCAACGCTTGTCAGTGTGGTCAAGCATTGCTTGGCTAAATTGGCATCGTCTTGGTAG
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; ORGANISM: Klebsiella
US-09-489-039A-5247
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US-09-489-039A-5247/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5247
LENGTH: 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5247, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 337; Conserv
                                                                                       1019
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                                                                                                                                                                                                                                                                                                                                                     686 CGATACTGCTGCAGCCCCAGCGGGTAGCGGTCCATATGGTCCTCAGTCACGTTGAGGATG
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                                                                                                                                              CCGACACCAACAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACAGTG
                 CGTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCT
                                                                                       ACATACAGCTCTCGATCGGTGTCCAGCAGCATC---AGCGCCGGCAGGCCGATATTGCCG
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ilarity 51.1%;
Conservative
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Pred. No. 3.9e-20;
0; Mismatches 289
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GENERAL INFORMATION:

APPLICANT: SHIGENOBU, SHUJI

APPLICANT: WATANABE, HIDEMI

APPLICANT: WATANABE, HIDEMI

APPLICANT: SAKAKI, YOSHIYUKI

TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYN

FILE REFERENCE: 081356/0159

CURRENT APPLICATION NUMBER: US/09/790,988

CURRENT APPLICATION NUMBER: JP2000-107160

PRIOR APPLICATION NUMBER: JP2000-107160

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1
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US-09-790-988-1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera sp
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                                                                                                                                                                                                                                                                                                                         240844 ATCAAGTATTTCTAGTACGGGAACACCTATATTACCACCTAGAAAAGCTTTATATCCTGA 240903
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                                                                                                                                                                                                                                                                                                                                                                                                                                 862 TGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCCACCAAATCCATATTTTGGAT
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                                    TCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGGCTGAGCTTAAGAGTTCACTGTC 1221
                                                                                                                                                               TGAAATAATAGGACAGGTCACTTCTCTAG-----
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ANATGAAGAAATACCCGGACTTATAACAATTAAGTCTGATTCTAGAATCCACTGATGGTC 241116
                                                                            GGCGATGATTGGTGTGTTTGTTGCTTGAGTTAGATCTCGTGCTTTGAGTGTATCAATGAA 1101
                                                                                                                                                                                                                                                                                  ATGITTTGCCATCTCGCCTACTAATGTCGTAACAGTGCTTTTGGCATTTGAGCCTGTGAT 1041
                                                                                                                   CAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTTTGGCGGCGACAATACTCGGCGT 1161
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Pred. No. 8e-14;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 640681
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NAME/KEY: misc_feature
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LOCATION: (B) LOCATION 1...1368
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SEQUENCE DESCRIPTION: SEQ ID NO: 1574:
US-09-107-532A-1574
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US-09-107-532A-1574/c
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    Matches
                     Query Match
Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1574: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
APPLICATION NUMBER: 00/001-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
APPLICATION NUMBER: 60/051571
PILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241237
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                                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1342 TCCAGAGCTGCCCAAACCGACGACGGCATATTTTT 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1222 CAAGCTGCCAAAATGACAATGAACGCCTGTGGGCAGTTTATCTGCCAAGGTAGGATTGGG
                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (781)893-50
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1368 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTGTTAAACCCCATTCCTAAAATTAATATTTTTT
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                6.0%;
53.6%;
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Score 83; DB 3;
Pred. No. 9.5e-15;
0; Mismatches 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAECIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and David Bush
AND AMINO ACID (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241272
                                        Length 1368;
  Indels
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Gaps
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RESULT 15
US-09-221-017B-881/c
; Sequence 881, Application US/09221017B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-7787
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US-09-252-991A-7787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7787, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
SEQ ID NO 7787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 567
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1009 TTGCTTTTGAATCATTATAAAATTTTCTGCCTTGGATTTCTCCTACATATTGCGTACGAT 950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 CCGTGCCAAGCCCATCAATTGCTGCAATGGTTGAGCCGATGTTTGTACCTTTTGAATCAT
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                                                                                                                                                                                                                                                                ACGCCTTCAGCGCGCCGAGCATGGCGTCGAACGGCAGGCCGACCGCATGGCCCAGCGCCA
                                                                                                                                                                                   GCGCGGCGAGCGCGTTGGAATAGTTGTGGGCGCCACGGATCTTCAGTTCGCCAACCGGCA
                                                                                                                                                                                                                    GTGCAGATAAGGCATTGAGTAGGTTATGCTTGCCTTTGATTTTAATTGATGGATTGGTA
                                                                                                                                                                                                                                                                                                     AAGTCTTAAGGGTATCAAGCATGGCATCCATGGGAAGATTGGCAGCTGTGCCTAAGGCAA
                                                                                                         GCAGCTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 69.8; DB 3;
Pred. No. 6.5e-11;
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Best Local Similarity
Matches 334; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/AU
PILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERALLING JALLAND OF WINDOWS VERSISOFTWARE: FASTSEQ for Windows VersiCURRENT APPLICATION DATA:
US/09/221,017B
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CORRESPONDENCE ADDRESS:
MORRISON & FOERSTER
MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: /5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27
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                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: 1...2402
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                                                                                                       2105
                          2045 ATTCTTAATATCCATAGCTTTGGCAGCAATGGCAGTTGCCATAGCATTGTGCCTGTTGTG
                                                                                                                                                                                   2165 GGTAGAATTTACGTTCGTAGCTTTGGAGTCATTGATATAATCGACACCCTTTACGCGAGC
                                                                                                                                415 AATATATTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGGGTATCAAGCATGGCATC
                                                             475 CATGGGAAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAGGTTATG
                                                                                                                                                                                                                      355 GGTTGAGCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATC
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                                                                                                                                                                                                                                                           Score 67; DB : Pred. No. le-09
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                                                                                                                                                                                                                                                                                DB 3; Length 2402; 
1e-09;
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1514 CATGGTTGTTGTTGTCTTGCCATTACTACCCGTGATGCACACCATAAATGCATCGGT 1458
                                                                                                                                                                                                                                             1634 GCTCAACTCTATTACATAATAAGGATGAGGATCGTAAGCGACCTGTCTGGCCAGACTAAA 1575
                                                                                                                                                                                                                                                                                                                                                                          1694 AATATTGAGCAGAATGGCCACATTAGCCCCTGAAGTCGTACATGTTGTCCCAGTTGAAAAACT 1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1814 AAAAGGATCATCCTCCCAGTAGATGAAGCAATCCTCGGGTTGCTGATTCCGAGTGATTCT 1755
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                                                                                                                                                                   946 GCCAATATTACCGCCGACACCAACATCATGCCTGCATGTTTTGCCATCTCGCCTACTAA 1005
                                                                                                                                                                                                                                                                                                          886 TGAÇAGCTCAAGCACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGGCGT 945
                                                                                                                                                                                                                                                                                                                                                                                                                             826 GAGATITAAAATTGITGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAAACT 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 715 TAAATTGGCATCGTCTTGGTAGATGATG-----GCGGTTTGGCAATTTTCAAAAATACG 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 655 TGTTGTGATAATGGTGTGATTTGGGGCAACGCTTGTCAGTGTGGTCAAGCATTGCTTGGC 714
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ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,076
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
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PRIOR PILING DATE: 2000-09-06
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PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,34
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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Remaining Prior Application data
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27195
LENGTH: 1398
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Mandio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                            APPLICATION NUMBER: 60/267,636
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Zyskind, Judith
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; ORGANISM: Moraxella catarrhalis
US-10-282-122A-27195
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Best Local Similarity 100.0%;
Matches 1380; Conservative 0
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                                                                       TGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCAC
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Pred. No. 0;
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Sequence 35, Application US/10672787

Publication No. US20040067554A1

GENERAL INFORMATION:
APPLICANT: LAGACE, Robert, E.
APPLICANT: BERG, Kim, L.
APPLICANT: BERG, Kim, L.
APPLICANT: BERG, Kim, L.
TITLE OF INVENTION: NUCLECTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME,
FILE REFERENCE: ELITRA.025C1
CURRENT APPLICATION NUMBER: US/10/672,787

CURRENT APPLICATION NUMBER: US/10/672,787

CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 09/596,002
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL Program
SEQ ID NO 35
LENGTH: 96109
TYPE: DNA
ORGANISM: Moraxella catarrhalis
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1380; Conservative 0; Mismatches
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                                                                                         GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA
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                     CAAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGACGACATATTTTTTTGA
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APPLICANT: Namudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kar
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Yemamocto, Robert
APPLICANT: Yemamocto, Robert
APPLICANT: Xu, H.
APPLICANT: NUMBER: 00/10/282,122A
CURRENT APPLICATION NUMBER: 60/291,078
PRIOR APPLICATION NUMBER: 60/291,078
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-10-2-16
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US-10-282-122A-8940/c
; Sequence 8940, Application US/10282122A
; Publication No. US20040029129A1
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LENGTH: 1344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Acinetobacter baumannii
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ilarity 52.4%;
Conservative
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Pred. No. 2.7e-53;
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                                                                                                                                              AGTTTATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGA 1315
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                                                                                               ATCTGATCGTGTCCGGGAGGTGTGGGGGCGGGAGTCCGTTACAGCAACTTGGTAGCCTTGT
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TCATGCAGGAAATTTACAGCAGAAACACCTGATATTCCCAAGCCTGCTACAACTTTT
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TITLE OF INVENTION: Identification of Essential Genes in TITLS OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-27
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-12-16
PRIOR PILING DATE: 2001-12-16
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US-09-815-242-7090/c
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7090
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Patent No. US20020061569A1
GENERAL INFORMATION:
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Best Local Similarity 49.6%;
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APPLICANT: Ohlsen, Ka
APPLICANT: Zyskind,
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TYPE: DNA
ORGANISM: Haemophilus influenzae
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NAME/KEY: CDS
LOCATION: (1)...(1314)
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301 CAATGCCAGTGATGATATGCCATAAACCGTGCCAAGCCCATCAATTGCTGCAATGGTTGA 360
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                                                                  TTGATTAATTAATTCAGCTAATTCTGAAAAATCAGCCCCTTTTCCGTCTCCGCCTAGCAA
                                                                                                        CTGCATAACATATGCTGACAGCTCACTAAAATCTTGACCTTTACCAAGCCCAAGCCCAAAAT
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Trawick, John D.
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Zyskind, Judith W.
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Pred. No. 1.4e-33;
0; Mismatches 606;
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RESULT 5
US-10-202-122A-22236/c
; Sequence 22236, Application US/10282122A
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; Remaining Prior Application data re
; NUMBER OF SEQ ID NOS: 78614
; SOBTWARE: PatentIn version 3.1
; SEQ ID NO 22236
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
US-10-282-122A-22236
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FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,12
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OR APPLICATION NUMBER: 60/230,347
OR FILLING DATE: 2000-09-09
OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
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  1026
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
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Forsyth, R.
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AGAGATAATCCACACAAGAAAGACCTGTTTTGCCAAGCCCGATGATAGTAATATTTTT
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Best Local Similarity
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LENGTH: 1314
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CURRENT APPLICATION NUMBER: US/10/958,216

CURRENT FILING DATE: 2004-10-04

RAIOR APPLICATION NUMBER: PUT/A03/00462

PRIOR FILING DATE: 2003-04-02

PRIOR PILING DATE: 2003-04-02

PRIOR APPLICATION NUMBER: 60/369,511

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PRIOR APPLICATION NUMBER: 60/385,089

PRIOR APPLICATION NUMBER: 60/385,751

PRIOR APPLICATION NUMBER: 60/385,751
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CANADIEN, VALLA
DOMAGALA, MEGAN
TOTISTON, SIMON
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TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTT
                                                  GAGACTTGCACAAGCAGGCGACAATAATACCA-----TATCTCCGCTTTGCAA
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VALLEE, FRANCOIS
VIRAG, CRISTINA
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PINDER, BENJAMIN
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CANADIEN, VERONICA
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VEDADI, MASOUD
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MCDONALD, MERRY-1
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                                                                                                GTGCGGTTTGAATTTCTGGTGTTTTTACCGCAAGCCCTGGGCTAATAACAATCATATCGC
                                                                                                                                         TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGGCTGATGATGTCTGATCGG
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TTTCAAGTAACCATTCCTGATTTAAACTACCAGTATGAAGAGGGATATTTTGAGGAAGTT
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US-09-754-468-44
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US-09-754-468-44/c
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LENGTH: 11498
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Publication No. US20050192237A1
GENERAL INFORMATION:
APPLICANT: Iversen, Patrick L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Antisense Antibacterial TITLE OF INVENTION: Composition and Method FILE REFERENCE: 0450-0033.30 CURRENT APPLICATION NUMBER: US/09/754,468 CURRENT FILING DATE: 2001-01-04 PRIOR APPLICATION NUMBER: US 60/174,484 PRIOR FILING DATE: 2000-01-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version
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Local Similarity 49.6%;
hes 683; Conservative
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CTGCATAACATATGCTGACAGCTCACTAAAATCTTGACCTTTTACCAAGCCCCACACCAAAAT
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                                                          AATACCTATAGCTTGTGCCAATGCTGTTGCTGCCAAAATGTTCATATAATTATGGCGACC
                                                                                        AAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAGGTTATGCTTGCC
                                                                                                                                        TTGAAAACGATGATCTAACCCTTTGAAATGACGAAGTGCGGTACGAATTGAATCTAAATT
                                                                                                                                                                                TTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGGGTATCAAGCATGGCATCCATGGG
                                                                                                                                                                                                                        CCCCACATTTGTTGCTTTAGAGTCATTAATCCAACGAATGCCATTAGCTTGATGCACTAA
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RESULT 8
US-10-329-670-1/c
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   FILE REFERENCE: PB186P1
CURRENT APPLICATION NUMBER: US/10/329,670
CURRENT FILING DATE: 2002-12-24
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
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                                                                                                                                                                                            Sequence 1, Application US/10329670
Publication No. US20040018503A1
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the
TITLE OF INVENTION: Thereof, and Uses Thereof
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SEQ ID NO 1
LENGTH: 1830121
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NAME/KEY: misc_feature
NAME/KEY: (9921)..(992
NAME/KEY: misc feature
LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals
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TYPE: DNA
ORGANISM: Haemophilus
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OTHER INFORMATION: n
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LOCATION: (44416)..(444
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LOCATION: (9921)..(9921)
OTHER INFORMATION: n equals
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NAME/KEY: misc feature
LOCATION: (10150)..(10150)
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NAME/KEY: misc_feature
LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals
          NAME/KEY: misc_feature
LOCATION: (51602)..(51602)
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NAME/KEY: misc_feature
LOCATION: (51334)...(51334)
OTHER INFORMATION: n equals
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LOCATION: (45593)...(45593)
OTHER INFORMATION: n equals
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LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals
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LOCATION: (44905)..(44905)
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals
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LOCATION: (36543)..(36543)
OTHER INFORMATION: n equal
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NAME/KEY: misc_feature
LOCATION: (29298)..(29298)
OTHER INFORMATION: n equal
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (131360)..(131360)
OTHER INFORMATION: n equals
                                          NAME/KEY: misc_feature
LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals
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LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals
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LOCATION: (122167)...(122167)
OTHER INFORMATION: n equals
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LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals
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LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals
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LOCATION: (119924)..(119924)
OTHER_INFORMATION: n equals
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LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals
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LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals
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LOCATION: (102696)...(102696)
OTHER INFORMATION: n equals
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LOCATION: (100091)...(100091)
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LOCATION: (65313)..(65313)
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LOCATION: (65309)..(65309)
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LOCATION: (119750). (119750)
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LOCATION: (80024)..(80
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NAME/KEY: misc_feature
LOCATION: (55369)..(55369)
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals
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LOCATION: (147197)..(147197)
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LOCATION: (145942)..(145942)
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LOCATION: (145171)...(145171)
OTHER INFORMATION: n equals
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LOCATION: (142750)..(142750)
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LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals
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LOCATION: (152530)..(152530)
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
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LOCATION: (145058)..(1
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Similarity 49.6%;
TTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGGGTATCAAGCATGGCATCCATGGG
                                                 CCCCACATTTGTTGCTTTAGAGTCATTAATCCAACGAATGCCATTAGCTTGATGCACTAA
                                                                       GCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATCAATATA
                                                                                                                 CAAATGCAATTTACCCTCAATATA-----AAGCCCAGCCAATGCAGCAACTGTACT
                                                                                                                                                                                TTGATTAATTAATTCAGCTAATTCTGAAAAATCAGCCCCTTTTCCGTCTCCGCCTAGCAA 1204158
                                                                                                                                                                                                           CGATGAAAATTTTGCAAGCAGCGCACCATCTCGACCAAAACAATAACAAATAATGTGTGG
                                                                                                                                                                                                                                                                           GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA
                                                                                                                                                                                                                                                                                                                                           TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTT
                                                                                                                                               CAATGCCAGTGATGATATGCCATAAACCGTGCCAAGCCCCATCAATTGCTGCAATGGTTGA
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Pred. No. 9.3e-32;
0; Mismatches 606;
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1204332

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1204380

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RESULT 9
US-10-18-865-1/c
; Sequence 1, Application US/10158865
; Publication No. US20040203093A1
; GENERAL INFORMATION:
       APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186P2C1D1
CURRENT APPLICATION NUMBER: US/10/158,865
                                                                                                                                                                                                                                                                                                 1203207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1203717 GGCGATAATCTTCTAAATCCATATAGCGATCCATATGATCTTCAGTCACGTTCAAGACAG
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                                                                                                                                                                                                                                                                                                                                 CCAAAAAATTCACAGCTGACAGTCCAGAGCTGCCAAAACCGACGACGACGATATTTTTT 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGATTGA 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTCAAGTAACCATTCCTGATTTAAACTACCAGTATGAAGAGGGATATTTTGAGGAAGTT 1203268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCGGTTTGAATTTCTGGTGTTTTTTACCGCAAGCCCTGGGCTAATAACAATCATATCGC 1203328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTT 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGACACCAACAATCATGCCTGCATGTTTTGCCATCTCGCCTAATGTCGTAACAGTGC
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                                                                                                                                                                                                                                                                                                                                                                                        TATCAATACCAGTAGGATTTTTTCGAGTATCAATCACACGAATATTAGCCTGTTGGGATA 1203208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGG 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATACCAACTTTCACACCAGCAGCTTTCGCCATTTCATAAACTAAAGTAGTTACGGTAC 1203481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGCTGCCGCAGCTTTTAAGCTATAAGTTGTCTCAAGCTGAAAACTAGAAAGCTCTAGTA 1203598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TATCTTCATTGTTCAACACACCTACTTTAGCATTATGATAAATGCGTAATTTTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTTTTCAAAAATACGCAATTTTTGTG
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                                                                            Haemophilus
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PRIOR APPLICATION NUMBER: US 09/557,884;
PRIOR FILING DATE: 2000-04-25;
PRIOR APPLICATION NUMBER: US 08/476,102;
PRIOR FILING DATE: 1995-06-07;
PRIOR APPLICATION NUMBER: US 08/426,787;
PRIOR FILING DATE: 1995-04-21;
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1;
SOFTWARE: PatentIn version 3.1
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NAME/KEY: misc_feature
NAME/KEY: misc_feature
136636)..(36
FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a,t,c,
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NAME/KEY: misc_feature
LOCATION: (47036)...(47036)
OTHER INFORMATION: n equals
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LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals
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LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals
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NAME/KEY: misc feature
LOCATION: (4747)..(4747)
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LOCATION: (45732)..(45732)
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LOCATION: (44905)...(44905)
OTHER INFORMATION: n equals
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LOCATION: (44416)..(44416)
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LOCATION: (40808)..(40810)
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OTHER INFORMATION: n equals
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LOCATION: (36543)...(36543)
OTHER INFORMATION: n equals
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LOCATION: (9921)..(9921)
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NAME/KEY: misc_feature
LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals
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LOCATION: (121344)...(121344)
OTHER INFORMATION: n equals
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LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals
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LOCATION: (119924)..(119924)
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LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals
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LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals
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LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals
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LOCATION: (100091)..(100091)
OTHER_INFORMATION: n equals a,t,c,
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LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals
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LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals
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LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (51786)...(51786)
OTHER INFORMATION: n equals
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LOCATION: (65313)..(65
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LOCATION: (65309)..(65
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature LOCATION: (152500)..(152500) OTHER INFORMATION: n equals
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LOCATION: (150841)...(150841)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (145942)...(145942)
OTHER INFORMATION: n equals
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LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals
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LOCATION: (145171)...(145171)
OTHER INFORMATION: n equals
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals
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LOCATION: (131360)..(131360)
OTHER INFORMATION: n equals
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals
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LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals
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301 CAATGCCAGTGATGATATGCCATAAACCGTGCCAAGCCCATCAATTGCTGCAATGGTTGA
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                                             TTGATTAATTCAGCTAATTCTGAAAAATCAGCCCCTTTTCCGTCTCCGCCTAGCAA
                                                                                                                                                                                                                                                                                 TAAACATTGAGCTAAATGCGTAAATTCTTCGCCGCGCTTTTCAAAAGAAGCAAACTGATC
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                                                                CGATGAAAATTTTTGCAAGCAGCGCACCATCTCGACCAAAACAATAACAAATAATGTGTGG 1204218
                                                                                                                                 GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA
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Pred. No. 9.3e-32;
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77	1320 CCAAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCCGACGACGACGACTTTTTTT 13
1319 1203208	1260 TATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGATTGA
1259 1203268	1200 CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGACAATGACGCCTGTGGGCAGTT
1199 1203328	1140 TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATGATCGGC
1139 1203388	1080 GTGCTTTGAGTGTATCAATGAACAATTGAACACTCGCTGATCACAGGAATGCCTTGAGCTT
1079 1203429	1020 TTTIGGCATITGAGCCIGTGAIGGCGAIGATTGGIGTGTITGTIGCTIGAGTTAGAICTC
1019 1203481	960 CGACACCAACAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACAGTGC
959 1203541	900 CCACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGGGGTGCCAATATTACCGC
899 1203598	840 TTGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCA
839 1203658	780 CCAAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGCGGAGAGATTTNAAATTG
779 1203718	720 TGGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTTTCAAAAATACGCAATTTTTGTG
719 1203775	660 TGATAATGGTGTGATTTGGGGCAACGCTTGTCAGTGTGGTCAAGCATTGCTTGGCTAAAT
659 1203807	601 ATCACCATCAACTAAATAAATAAAATCTGC-CGTTTGGTGGCTAAGTAAGCTATTTGTTG
600 1203867	541 TITGATITTTAAITGATGGATTGGTAAAAGTTTGITTTTTTGATGATATAAIGCCATACC
540 1203927	481 AAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTTATGCTTGCC
1203987	421 TTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGGGTATCAAGCATGGCATCCATGGG
420 1204047	361 GCCGATGTITGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATCAATATA 420
1204107	1204157 CAAATGCAATTTACCCTCAATATAAAGCCCAGCCAATGCAGCAACTGTACT

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Sequence 1, Application US/10981687
Publication No. US20050131222A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleotide Sequence of the Hae
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186P2C1D12
CURRENT APPLICATION NUMBER: US/10/981,687
CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: US 10/158,865
PRIOR APPLICATION NUMBER: US 09/557,884
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: US 08/476,102
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SEQ ID NO 1
LENGTH- 1830121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (9921).. (9921)
OTHER INFORMATION: n equals a
FEATURE:
NAME/KEY: misc_feature
LOCATION: (10150).. (10150)
OTHER INFORMATION: n equals a
FEATURE:
NAME/KEY: misc_feature
LOCATION: (29298).. (29298)
OTHER INFORMATION: n equals a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1
LENGTH: 1830121
TYPE: DNA
ORGANISM: Haemophilus influenzae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4747). (4747)
OTHER INFORMATION: n equals a,t,c,
FEATURE:
FEATURE:
                   NAME/KEY: misc_feature
LOCATION: (44975). (44975)
OTHER INFORMATION: n equals a.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (45593). (45593)
OTHER INFORMATION: n equals a.
FEATURE:
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NAME/KEY: misc_feature
LOCATION: (44416)..(44416)
OTHER INFORMATION: n equals a
FEATURE:
NAME/KEY: misc_feature
LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals a
FEATURE:
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NAME/KEY: misc feature
LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a
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NAME/KEY: misc feature
LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals a
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NAME/KEY: misc_feature
LOCATION: (36551)...(36551)
OTHER INFORMATION: n equals
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LOCATION: (36543)...(36543)
OTHER INFORMATION: n equal
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LOCATION:
OTHER INFO
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (121344)..(121344)
                                     NAME/KEY: misc feature
LOCATION: (120038)...(120038)
OTHER INFORMATION: n equals
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LOCATION: (119724)..(119924)
OTHER INFORMATION: n equals
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LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals
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NAME/KEY: misc feature
LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (100091)...(100091)
OTHER INFORMATION: n equals
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LOCATION: (65313)..(65313)
OTHER INFORMATION: n equals
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LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals
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LOCATION: (55369)..(55369)
OTHER INFORMATION: n equal
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LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals
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LOCATION: (51602)...(51602)
OTHER INFORMATION: n equal
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NAME/KEY: misc feature
LOCATION: (80024)...(80024)
OTHER INFORMATION: n equals
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LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equal
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LOCATION: (105121)..(105121)
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Best Local :
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
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LOCATION: (147197)..(14
OTHER INFORMATION: n ec
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NAME/KEY: misc_feature
LOCATION: (145058)..(145058)
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LOCATION: (142750)..(142750)
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LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals
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LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals
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LOCATION: (145171)..(1:
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LOCATION: (131360)..(131360)
OTHER INFORMATION: n equals
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LOCATION: (131340)...(131340)
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Sequence 569, Application US/10795159
Publication No. US20050221439A1

GENERAL INFORMATION:
APPLICANT: BAKALETZ et al.
TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE
FILE REFERENCE: 28335/38815A
CURRENT APPLICATION NUMBER: US/10/795,159
CURRENT FILING DATE: 2004-03-05
PRIOR APPLICATION NUMBER: US 60/453,134
PRIOR FILING DATE: 2003-03-06
APRIOR FILING DATE: 2003-03-06
NUMBER OF SEQ ID NOS: 771
SOFTWARE: Patentin version 3.2
SEQ ID NO 569
LENGTH: 14324
TYPE: DNA
TYPE: DNA
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TYPE: DNA
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Best Local Similarity
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US-10-795-159-685/c; Sequence 685, Application US/10795159; Publication No. US20050221439A1
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SEQ ID NO 685
LENGTH: 908766
TYPE: DNA
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TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE FILE REFERENCE: 2835/38815A

CURRENT APPLICATION NUMBER: US/10/795,159

CURRENT FILING DATE: 2004-03-05

PRIOR APPLICATION NUMBER: US 60/453,134

PRIOR FILING DATE: 2003-06

NUMBER OF SEQ ID NOS: 771
                                                                                                                                           NAME/KEY: misc feature LOCATION: (9223)..(9223) OTHER INFORMATION: n is
NAME/KEY: misc_feature
LOCATION: (292404)..(292404)
OTHER INFORMATION: n is a, c
FEATURE:
                                                                            NAME/KEY: misc feature
LOCATION: (39640)...(39640)
OTHER INFORMATION: n is a,
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; NAME/KEY: misc_feature; LOCATION: (908604)..(908641); OTHER INFORMATION: n is a, c, US-10-795-159-685
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                                                                                               ATTACCGCCGACACCAACCAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGT
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Pred. No. 2.9e-30;
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RESULT 13
US-10-282-122A-25165/c
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PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PELICATION NUMBER: 60/230,347
PRIOR PELICATION NUMBER: 60/230,347
PRIOR PELICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PELICATION NUMBER: 60/242,578
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
                        Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25165
LENGTH: 1281
TYPE: DNA
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FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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  ORGANISM: Legionella
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                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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Zyskind, Judith
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Malone, Cheryl
Haselbeck, Robert
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Trawick, John
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               RESULT 14
US-10-958-216-402/c
; Sequence 402, Application US/10958216
; Publication No. US20050181388A1
; GENERAL INFORMATION:
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Pred. No. 1.9e-31;
0; Mismatches 412;
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CURRENT APPLICATION NUMBER: US/10/958,216

CURRENT FILING DATE: 2004-10-04

PRIOR APPLICATION NUMBER: PCT/CA03/00462

PRIOR FILING DATE: 2003-04-02

PRIOR APPLICATION NUMBER: 60/369,511

PRIOR FILING DATE: 2002-04-02

PRIOR PRIOR DATE: 2002-04-02

PRIOR APPLICATION NUMBER: 60/385,089

PRIOR FILING DATE: 2002-05-31

PRIOR FILING DATE: 2002-05-31
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 678; Conserv
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SEQ ID NO 402
LENGTH: 1314
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Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 1132
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FILING DATE: 2002-06-04
APPLICATION NUMBER: 60/386,553
FILING DATE: 2002-06-05
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CANT: VIRAG, CRISTINA
OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM BACTERIA
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APPLICATION NUMBER: 60/386,367
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PINDER, BENJAMIN
RICHARDS, DAWN
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITEA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/207,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
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US-10-282-122A-30713/ Application US/10282122A
Publication No. US20040029129A1
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US-10-282-122A-30713
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Best Local Similarity
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Wall, Daniel
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1: /SIDSS/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

2: /SIDSS/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

3: /SIDSS/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

4: /SIDSS/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

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10: /SIDSS/ptodata/2/pubpna/USO1_NEW_PUB.seq:*

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16: /SIDSS/ptodata/2/pubpna/USO1_NEW_PUB.seq:*

16: /SIDSS/ptodata/2/pubpna/USO0_NEW_PUB.seq:*

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US-10-1467-657-7645

US-10-793-626-655

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Sequence 220, App
Sequence 205, App
Sequence 205, App
Sequence 10002, A
Sequence 8739, Ap
Sequence 655, App
Sequence 3574, Ap
Sequence 1328, Ap
Sequence 1328, Ap
Sequence 1328, Ap
Sequence 1340, Ap
Sequence 10005, Ap
Sequence 10005, Ap
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ALIGNMENTS

US-11-194-246-220/c; Sequence 220, Applic; Publication No. US20; GENERAL INFORMATION:

Application US/11194246 o. US20050272089A1

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; LENGTH: 2925
; TYPE: DNA
; ORGANISM: ARTIFICIAL
                                                                                                                                                                          Query Match 11.6
Best Local Similarity 49.6
Matches 683; Conservative
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APPLICANT: Trepod, Catherine
APPLICANT: Trepod, Catherine
APPLICANT: Trepod, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAB AND PITLE OF INVENTION: USE
FILE REFERENCE: 00592 US1 (Mar 268.05920101)
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR PILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: Patentin version 3.0
                                                                          2240 TAAACATTGAGCTAAATGCGTAAATTCTTCGCCGCGCTTTTCAAAAGAAGCAAACTGATC 2181
61 CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA 120
                                                                                                                    TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC 60
                                                                                                                                                                                                       11.6%;
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                                              TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGG
                                                                                                                                             GTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTT
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                                                                                               -GAATAATTCAATATCGCCGATTACTTCCACTCCCGCTTTAA
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APPLICANT: Trepod, Catherine
APPLICANT: Arvidson, Staffan
ITILE OF INVENTION: CRITICAL GENES AND POLYPEPT
ITILE OF INVENTION: USE
FILE REFERENCE: 00592.US1 (M&R 268.05920101)
CCURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2002-10-19
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: Patentin version 3.0
SEQ ID NO 205
LENGTH: 2850
TYPE: DNA
ORGANISM: ARTIFICIAL
FRATURE
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US-11-194-246-205/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.6%;
Best Local Similarity 54.0%;
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 205, Application US/11194246 Publication No. US20050272089A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mott,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                          GCTGATCACAGGAATGCCTTGAGCTTTGGCGGCGACAATACTCGGCGTTCTTGGGTTAAT
GCCGATTACTTCCACTCCCGCTTTAAGTGCGGTTTGAATTTCTGGTGTTTTTACCGCAAG
                                                                                                                                TGTGTTTGTTGCTTGAGTTAGATCTCGTGCTTTGAGTGTATCAATGAACAATTGAACATC
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Pred. No. 5.1e-25;
0; Mismatches 257;
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APPLICANT: Trepod, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF
TITLE OF INVENTION: USE
FILE REFERENCE: 00592.US1 (M&R 268.05920101)
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR APPLICATION NUMBER: US/00/345,438
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID MOS: 621
SOFTWARE: PatentIn version 3.0
TYDE: DNA
TYPE: DNA
TYPE: DNA
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US-11-194-246-225/c
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Best Local Similarity
Matches 337; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 225, Application US/11194246 Publication No. US20050272089A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mott, John APPLICANT: Trepod, Ca APPLICANT: Arvidson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: ARTIFICIAL
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 CTTTGTCGCTGCGCG-
                         TGTGTTTGTTGCTTGAGTTAGATCTCGTGCTTTGAGTGTATCAATGAACAATTGAACATC 1113
                                                                                 CTCGCCTACTAATGTCGTAACAGTGCTTTTTGGCATTTGAGCCTGTGATGGCGATGATTGG
                                                                                                                                         AAGTGCAGGCGTGCCAATATTACCGCCGACACCAACAATCATGCCTGCATGTTTTGCCAT
                                                                                                                                                                                                              AAGCTGAAAACTTGACAGCTCAAGCACCACCAAATCCATATTTTGGATCGTTAATAATTC
                                                                                                                                                                                                                                              ATGATCTTCAGTCACGTTCAAGACAGTCGCTGCCGCAGCTTTTAAGCTATAAGTTGTCTC
                                                                                                                                                                                                                                                                           ATGATCAGCGGAGAGATTTAAAATTGTTGCCCCCTTGAGCTGCCAAATTTGAGATATGCTC
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                                                                                                                    CAAAGCGGGAATCCCAATATTTCCGCCCATACCAACTTTCACACCAGCAGCTTTCGCCAT
                                                                                                                                                                                  AAGCTGAAAACTAGAAAGCTCTAGTACATAAAGTTCACAATCTTCATTC---AACAATGA
                                                                                                                                                                                                                                                                                                          ATTATGATAAATGCGTAATTTTGCTTGGCGATAATCTTCTAAATCCATATAGCGATCCAT 5567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGCCCGATGATAGTAATATTTTT 2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAAGAGGGATATTTTGAGGAAGTTTATCAATACCAGTAGGATTTTTTCGAGTATCAAT
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                                                                                                                                                                                                                                                                                                                                                                                      9.6%;
                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No. 6.4e-25;
0; Mismatches 257;
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PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10002
LENGTH: 1323
TYPE: DNA
TYPE: DNA
ORGANISM: Lawsonia intracellularis
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US-11-098-686-10002/c
US-11-098-686-10002/c
; Sequence 10002, Application US/11098686
; Publication No. US20060024696A1
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APPLICANT: Kapur, Vivek and Gebhart, Connie J.

TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES

TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING

FILE REFERENCE: 09531-128001

CURRENT APPLICATION NUMBER: US/11/098,686

CURRENT FILING DATE: 2005-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US03/31318 PRIOR FILING DATE: 2003-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           754 ATTTTCAAAAATACGCAATTTTTGTGCCAAATAATCCACCATGCCATCGTGCCGATCAAG 813
TTTTTCATTAGACAACTGATACCATGCTAGTTCTGT 331
                                                        TEGTETETTECTTEAGTTAGATCTCGTGCTTT
                                                                                                                                                                           CATCTCGCCTACTAATGTCGTAACAGTGCTTTTTGGCATTTGAGCCTGTGATGGCGATGAT 1050
                                                                                                                                                                                                                                         TTCTGATAGTGGAGTTCCAATATTACCACCAACAAAAACACTTATACCTTGTTCTACCAA
                                                                                                                                                                                                                                                                                              TTCAAGTGCAGGCGTGCCAATATTACCGCCGACACCAACAATCATGCCTGCATGTTTTGC
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                                                                                                                   CATTGCTGCACATAAACTTGCTATAGTTGTTTTCCCCATTGGTCCCTGTTATGGCAATGAC
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54.2%;
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Pred. No. 1.6e-10;
0; Mismatches 151;
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Sequence 8739, Application US/11098686

Publication No. US20060024696A1

GENERAL INFORMATION:
APPLICANT: Kapur, Vivek and Gebhart, Connie J.
APPLICANT: KAPUR, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS
FILE REFERENCE: 09531-128001

FILE REFERENCE: 09531-128001

CURRENT APPLICATION NUMBER: US/11/098,686

CURRENT APPLICATION NUMBER: US/11/098,686

CURRENT FILING DATE: 2003-10-01

PRIOR APPLICATION NUMBER: US/0/416,395

PRIOR APPLICATION NUMBER: US/0/416,395
                                                                                                                                                                                                                                                                                                  RESULT 6
US-10-467-657-7645/c
US-10-467-657-7645/c
; Sequence 7645, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
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SOFTWARE: SeqWin99,
SEQ ID NO 7645
LENGTH: 1335
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 8739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                       CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
                                                                                                                                                                                    APPLICANT: CHIRON SPA
APPLICANT: FONTANA MARIA RITA
APPLICANT: FIZZA MARIAGRAZIA
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND
                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Lawsonia intracellularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1457619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGTGTGTTTGTTGCTTGAGTTAGATCTCGTGCTTT 1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTTCATTAGACAACTGATACCATGCTAGTTCTGT 1355889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATTGCTGCACATAAACTTGCTATAGTTGTTTTCCCATTGGTCCCTGTTATGGCAATGAC 1355925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATCTCGCCTACTAATGTCGTAACAGTGCTTTTGGCATTTGAGCCTGTGATGGCGATGAT
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                                                           version 1.04
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                                                                                                                                                                                          NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND METHODS OF USING
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; ORGANISM: Neisseria gonorrhoeae US-10-467-657-7645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 655, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
                                                                                                                                                                                                                                            Matches 101;
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 655
LENGTH: 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1037 AAGAGCG
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486 TGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTTAGGCTTATGCCTTTGA
                                                                                                              426 AGCGATGCGGTAGCCCTTTGAAAGTCTTAAGGGTATCAAGCATGGCATCCATGGGAAGAT 485
                                                                                                                                                                                                 366 TGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATCAATATATTCAC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       812 AGCGGGATGTCTTGCGTAGAAATCAAATCTTCATTGCCTTGTTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 TIGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAGGTTATGCCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              932 ACACGGTGCGGCAAGCCTTGGAAGGTTTTGACGTGTTCCAGCAATGCTTCGCGCGGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 GCCAGTGATGATATGCCATAAACCGTGCCAAGCCCATCAATTGCTGCAATGGTTGAGCCG
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                                                                     GTCTATGATCAATACCGGAAAAAGTAACAAGACTATCTACAATAGCTTTGACTGGCACTC
                                                                                                                                                      TATTAGTTGCTTTTGAATCATTATAATATTTTTTTTGTGCGATTTGTACCAATATACTGAA
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                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                   Description of Artificial nucleic acid sequence
                                                                                                                                                                                                                                                                  3.5%;
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Pred. No. 0
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Pred. No. 8.3e-07;
0; Mismatches 189;
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                                                                                                                                                                                                                                                                                                                                                                        Sequence:
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                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                    Length 1188;
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RESULT 8
US-10-793-626-3574
; Sequence 3574, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
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                                                            NUMBER OF SEQ
SEQ ID NO 1328
LENGTH: 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 3574
                                                                                                  APPLICANT: GATY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH00-03DIVZ
CURRENT APPLICATION NUMBER: US/11/079,463
CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR FILING DATE: 2000-04-04
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  Sequence 1328, Application US/11079463
Publication No. US20060073161A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                             TYPE: DNA
ORGANISM: B.fragilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
NAME/KEY: unsure
                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                               546
                                                                                                                                                                                                                                                                                                                                                                                                                                              419
                                                                                                                                                                                                                                                                                                                                                                                  479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486 TGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAAGGTATGCTTTGCCTTTTGA
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                                                                                                                                                                                                                                                                                                                                                                                GCACTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                             TTTTTAATT
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                                                                                             ID NOS: 10444
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                                                                                                                                                                                                                                                                                                                                                                                487
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Pred. No. 0.029;
0; Mismatches
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US-11-098-686-8219/c
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Best Local Similarity
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; ORGANISM: Lawsonia intracellularis US-11-098-686-8219
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; OTHER INFORMATION: Identity of nucleotide sequences at the above US-11-079-463-1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8219
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8219, Application US/11098686 Publication No. US20060024696A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/416,395 PRIOR FILING DATE: 2002-10-04
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                                                                                                 902 ACCAAATCCATATTTTGGATCGTTAATA---ATTCAAGTGCAGGCGTGCCAATATTACCG 958
                                                                                                                                                                                  842 GCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCACC
                                                                                                                                                                                                                                                            196 ATATATTCATCCATATTTCTATGGTAATCCAAATGATTTATAGAAATATTAGAACATATA
                                                                                                                                                                                                                                                                                                            782 AAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGCGGAGAGATTTAAAATTGTT
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CCGACACCAACAATCA 974
                                                                                                                                                       GCTATATCAGGACGAAATAGTGAACATGTCTGAAGTTGAAACTTGAAAGTTCTAAAAACA
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Pred. No. 0.37;
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RESULT 11 US-11-045-004-1 밁

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US-11-045-004-1
Query Match
Best Local Similarity 50.2
Matches 104; Conservative
                                                                                                             SEQ ID NO 1
LENGTH: 2944528
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                                                                                                                                                         PRIOR FILING DATE: 2000-04.
NUMBER OF SEQ ID NOS: 2854
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES FILE REFERENCE: 05394.0018-02 CURRENT APPLICATION NUMBER: US/11/045,004 CURRENT FILING DATE: 2005-01-28
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                                                                                                                                           SOFTWARE: PatentIn
                                                                             TYPE: DNA ORGANISM: Listeria monocytogenes
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                                                                                                                                                                                                    APPLICATION NUMBER: PCT/FR01/01118 FILING DATE: 2001-04-11
                                                                                                                                                                                                                                  APPLICATION NUMBER: 10/257,023 FILING DATE: 2002-10-08
                                                                                                                                                                                       APPLICATION NUMBER: FR 00/04,629
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 10/637,657
                                                                                                                                                                                                                                                                  FILING DATE:
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ROSE, MATTHIAS
VOSS, HAMUT
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GOMEZ-LOPEZ, NURIA
MADUENIO, ENCARNA
PABLOS, BETRIZ DE
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KARST, UWE
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PEREZ-DIAZ, JOSE-CLAUDIO
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CHARBIT, ALAIN
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HAIN, THORSTEN
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VAZQUEZ-BOLAND, ANTONIO
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KREFT, JURGEN
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                  3.1%; Score 42.2;
50.2%; Pred. No. 11
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   Mismatches 103;
                                 DB 18;
    Indels
                               Length 2944528;
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SEQ ID NO 3540
LENGTH: 4010
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local S
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
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                                                                                                                                                                                                                                                                   162 TAATTGAAAAGATGATAATTCTGTTATTAAATACTCATCTGATTTAACTTCTTGTGCAAC 221
                                                                                                                                                                                                                                                                                                                874 AAGCTGAAAACTTGACAGCTCAAGCACCACCAAATCCATATTTTTGGATCGTTAAT---AA
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                                                                                                                                                                                                                                                                                                                                                                                                  814 ATGATCAGCGGAGAGATTTAAAATTGTTGCCCCTTGAGCTGCCAAATTTGAGATATGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 754 ATTITCAAAAATACGCAATTITTGTGCCAAATAATCCACCATGCCATCGTGCCGATCAAG 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                            TGGTG 1055
                                                                                       AATATCACCGATTAGTGAAGTGACAGTAGTTTTACCGTTAGTTCCAGTAACTGCTATGAT
                                                                                                                                                                              TTTTGAGGCTACATAACCAATATTCCCAGAAAGTCGTCCAGTCAACACGCTTTTTTGGAA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAGGCATTGAGTAGGTTATGCTTGCC 540
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346
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Pred. No.
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RESULT 13 US-11-098-686-10005/c ; Sequence 10005, Application US/11098686 ; Publication No. US20060024696A1

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                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4356, Application US/10793626 Publication No. US20050255478A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FRANCSEQ for Windows Version 4.0
SEQ ID NO 10005
LENGTH: 1362
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SEQ ID NO 4356
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYBEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR PILING DATE: 2002-10-04
PRIOR FILING DATE: 2002-10-04
PRIOR FILING DATE: 2002-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 3444
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  318
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                                       65 CTAGCACAAGCAGGTGACAAAAGCACAGC 93
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CTTGCACAAGCTGGTGATAATAGAACAAC 290
                                                                                   GCTCGGAATCTATCGATAAACTTCTCACCACGTTCTTCAAATGTATGATACTGATCCCAA 319
                                                                                                                         GCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATCCATG
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Pred. No. 3.4;
0; Mismatches
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Pred. No. 6.7;
0; Mismatches 31;
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RESULT 15

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US-10-750-185-47750
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LENGTH: 3500
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Publication No. US20050260603A1
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APPLICANT:
APPLICANT:
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NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MMI GENOMICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                               1108 ATAGGTCTGACCTCATCCATTGAAGCCCTTAAGAGAAAAATACTGAGATTCCCTGAGAAA 1167
                                                                                                                                                                                                                                                 1048 GATGTGACTAACATTTAAATCACTAGACTTTGAGTAAAGACAATTATCTTCCATAATGTA 1107
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                                                                                                                       484 ATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAGGTTATGCTTGCCT 541
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                                                                                                                                                                                                                                                                                                                               91;
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Similarity 51.1%;
                                                                                 GAAGTGCTCTGACTCTAATTTGCCTTCAGAGTCAGTACTGCTACATTAGCTCTTCCCT
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HOLM, Tom
BATES, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DeNISE, Sue K.
KERR, Richard
                                                                                                                                                                                                                                                                                                                               Conservative
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Chan, Christina

Sent:

Tuesday, May 16, 2006 3:51 PM

To:

Graser, Jennifer; STIC-Biotech/ChemLib

Subject:

RE: rush search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

-----Original Message-----

From:

Graser, Jennifer

Sent:

Tuesday, May 16, 2006 2:43 PM ·

To: Subject: Chan, Christina rush search

Hi Christina,

Will you please authorize the following rush search a special case which is due?

Thanks,

Jennifer

STIC:

Please search oligonucleotides of at least 22 nucleotides in length from 11357 to 12736 of SEQ ID NO: 35 from application 10/672787 in pending and commercial databases.

Thanks,

Jennifer Graser Primary Examiner Art Unit 1645 REM 3B09 2-0858

THEORING 2005

Searcher:	
Searcher Phone:	
Date Searcher Picked up:	
Date completed:	
Searcher Prep Time:	_
Online Time:	

Type of Search										
NA# AA#:										
S/L: Oligomer:										
Encode/Transl:										
Structure #:Text:										
Inventor	Litigation:									

endors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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Minimum DB
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seq length: 2000000000
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1: geneseqn198
2: geneseqn199
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C 16 154.4 11.2 349980 C 17 152.8 11.1 1281	16 154.4 11.2		15 154.4 11.2 14324	14 157.6 11.4 110000	13 157.6 11.4 110000	c 12 160.4 11.6 110000	c 11 160.4 11.6 110000	c 10 160.4 11.6 2925	9 160.4 11.6		7 160.4 11.6	6 160.4 11.6	5 226.2 16.4	4 231 16.7	_	2 1380 100.0 96109	c 1 1380 100.0 1398	Result Query No. Score Match Length	, ap
14 AEB39164	8 ACA37295	13 ADT05649	13 ADT05533	14 AEB42401_28	14 AEB39175_30	2 AAT42063_12	2 AAT42063_11	15 AEE31251	14 AEC10868	11 ADL46439	8 ACA34366	4 AAS53453	9 ADA29995	8 ACA21070	12 ADL02987	4 AAF28548	8 ACA39325	DB ID	
Aeb39164 L. pneumo	Aca37295 Prokaryot	Adt05649 Haemophil	Adt05533 Haemophil	Continuation (29 o	Continuation (31 o	Continuation (13 o	Continuation (12 o	Aee31251 Haemophil	Aec10868 Haemophil	Adl46439 aspartate	Aca34366 Prokaryot	Aas53453 Haemophil	Ada29995 DNA encod	Aca21070 Prokaryot	Adl02987 DNA encod	Aaf28548 Genomic f	Aca39325 Prokaryot	Description	

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C, Haselbeck R, Ohlse J, Yamamoto R, Forsyt useful for identifying required for cellular for rational drug disco	Sq.	ALIGNMENTS BP. 20982. ssential gene; cell	AEB42737_15 ADL46441 AEC10870 AEB3719 ACA42843 AAS52295 ACA42843 AAS52295 AEE31236 ACB231256 ADF02545 ACCA44759 ACCA44759 ACCA44759 ACCA42598 ABD09098 ABD090987 ACA45545 ACCA471311 ACA53404 ACA51113 AAS89616 AAS89616 AAS89616 AAS9971862 ACF71662 ACF71662 ACF67367_48 ACF67367_48 ACF65387_0
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CC The invention relates to an isolated nucleic acid comprising any one of cthe 6213 antisense sequences given in the specification where expression co of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid cenciding a polypeptide whose expression is inhibited by the antisense cutleic acid; (2) a host cell containing the vector; (3) an isolated contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular contiseration; (7) identifying a compound that influences the activity of a gene in an operon required for centurized for proliferation, or that has an activity against a biological pathway contisered for century in which a proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological cor a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene compound's activity; (12) determining the extent compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required correctly programs, or for screening candidate molecules for rational correctly programs. The antisense and antiscover succession activity activity of screening backets molecules for rational contents of the carget of a condidate molecules for rational contents of the carget of the carget acids are useful for the ca
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04-APR-2001

(first entry)

Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.

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Moraxella catarrhalis

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 96109 BP; 28783 A; 18910 C; 20341 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
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ADL02987 standard;

06-MAY-2004 (first

encoding ដ M. catarrhalis protein #673.

gene; Moraxella catarrhalis;

Moraxella catarrhalis

06-JAN-2004

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Best Local Similarity 99.0
Matches 1374; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding a Moraxella catarrhalis polypeptide, preparing a composition for diagnosing, preventing or treating caused by Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid encoding an Moraxella catarrhalis polypeptide. The nucleic acid is useful for preparing a composition for diagnosing, preventing or treating infection caused by Moraxella catarrhalis. The present sequence represents DNA encoding a M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1410 BP; 409 A; 307 C; 302 G; 392 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catarrhalis protein.
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P-PSDB; ADL04907.
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                                               AAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAGGTTATGCTTGCC
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RESULT 4
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ID ACA210
XX ACA 21-MAR-2002; 2002WO-US009107. WO200277183-A2 Acinetobacter baumannii Antisense; ds; drug design; g Prokaryotic essential 19-JUN-2003 ACA21070 ACA21070 standard; (first prokaryotic DNA; entry) gene 1344 essential #2727 ВP gene;

cell

proliferation;

21-MAR-2001;

2001US-00815242

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08-FEB-2002;
06-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1344 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           format directly from WIPO at
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0; Mismatches
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Pred. No. 1e-55;
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                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for presents equence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; SEQ ID NO 1282; 328pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; Acinetobacter baumannii; bacterial disease;
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                GTTGACACAGCTCGACAGCTTCTTTAAGCGTTGCTGCATGTAAAATTTTAGTTGCGCCCT-
                                                                                                                               AAACTTGCACATGCTGGTGAT-----AGCAATACCACATCTTCAGCTTGTGTTTCAC
                                                                                                                                                        ATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAAT
                                                                                                                                                                                      AACGAATTGACGCAGGCAACAAACTGCTGACCACGGTCATTATAACTTTTAAACATATCA
                                                                                                                                                                                                        AAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAAATTTTTAAATTTGATCC
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2.5e-54;
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                                                                                                                                                                       GCTTTGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGA 1195
                                                                                                                                                                                                                                                                                    CCGCCGACACCAACCATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACA 1015
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                                                                                                                TCGGCTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGAACGAATGAACGCCTGTGGGC 1255
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                               ATCTGATCGTGTCCGGGAGGTGTGGGGGCGGGAATCCGTTACAGCAACTTGGTAGCCTTGT
                                                       AGTTTATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGA 1315
                                                                                      TCTGCTTGTAATĀATĀATTCTTGATCAĀGCTGACCĀĀĀĀCTGGTTTTAACACCAGCCGGA 210
                                                                                                                                            GCAATAGCTGCCTGAATTTCCGGTAATTGTGGTGCAAGGCCTGGGCTTAAAATAATCTCT
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RESULT 6
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AASS3453;

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DT 13-FEB-2002 (first
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DE Haemophilus influenz
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21-MAR-2000; 2000US-
PR 23-MAY-2000; 2000US-
PR 23-BC-2000; 2000US-
PR 23-MAY-2000; 2000US
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                                                                                                                                                                                                                        The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the genes, CC their use in the discovery of novel antibiotics, the essential genes, CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also cu useful for the identification of potential new targets for antibiotic CC development. The antisense nucleic acide can also be used to identify CC proteins used in proliferation, to express these proteins, and to obtain CC antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The cc antisense nucleic acid sequence is also useful to screen for homologous cucleic acids which are required for cell proliferation in a wide variety CC of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this pattent CC did not form part of the printed specification, but was obtained in CC electronic format directly from MIPO at
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                                                                       Query Match
Best Local S
Matches 683
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P-PSDB; AAU35594.
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                                                                         683;
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TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC
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Xu HH;
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drug design.
                                                                                                                                                             403 A; 214 C; 294 G; 403 T; 0 U; 0 Other;
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                                                                     Pred. No. 2.5e
D; Mismatches
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Pred. No. 2.5
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation, (8) identifying a gene required for cellular proliferation or the biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001; 2001US-00815242

06-SEP-2001; 2001US-00948993

25-OCT-2001; 2001US-0342923P

08-FEB-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an conganism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antiense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in effective in the printed specification, but was obtained in
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UDP-N-acetylpuyruvoylglucosamine reductase;
UDP-N-acetylglucosamine pyrophosphorylase;
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Query Match
Best Local Similarity
Matches 683; Conserv

Conservative

11.6%;

Score 160.4; DB 11; Pred. No. 2.5e-35; 0; Mismatches 606;

Indels Length 1314

89;

Gaps

DB 11;

1308

61

CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA TAAACATTGAGCTAAATGCGTAAATTCTTCGCCGCGCTTTTCAAAAGAAGCAAACTGATC TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC

-TATCTCCGCTTTGCAA

1201 120 1249 60

GAGACTTGCACAAGCAGGCGACAATAATACCA

TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTT 180

TGTTGGGCGTAAAAATTCTATCGCTTGTTCCATTGTATCGAACAA----

ATAACTTTG

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The invention relates to isolated, recombinant polypeptides (I) that have CC at least one activity of specified bacterial enzymes involved in cell CC membrane biogenesis. (I) are: UDP-N-acetylglucosamine 1-carboxyvinyl CC transferase-1 of Streptococcus pneumoniae (S.p.), Pseudomonas aeruginosa (C (P.a.) or Staphylococcus aureus (S.a.); CTP:CMP-3-deoxy-D-manno-CC octulosonate transferase of Escherichia coli (E.c.) or Haemophilus CC influenzae (H.i.); UDP-N-acetylmuramylalanyl-D-glutamate- 2,6-CC or P.a.; D-alanine-D-alanine-D-alanine-D-alanine-D-alanine-D-alanine-D-alanine-D-alanine-D-alanine-D-alanine-D-alanine-D-alanine-D-alanine-D-alanine-D-alanine-D-alanine-D-A-CC ox P.a.; D-N-N-CC acetylpuyruvoylglucosamine reductase of E.f., H.i. or S.a.; UDP-N-CC acetylpuyruvoylglucosamine pyrophosphorylase of E.f., H.i. or S.a.; UDP-N-CC acetylmuramate-alanine-D-glutamate-ligase of E.g.; and aspartate semialdehyde CC dehydrogenase of H.i and UDP-N-acetylmuramoylalanyl-D-glutamate (sic) of CC in the structural coordinates of (I), and these than used to design modulators of (I), potential therapeutic agents for treating CC diseases caused by the specified bacteria. This sequence represents a DNA
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08-ApR-2002;

09-ApR-2002;

09-kpR-2002;

19-kpR-2002;

11-MAY-2002;

01-kUG-2002;

06-NOV-2002;

06-NOV-2002;

24-DEC-2002;

24-DEC-2002;

24-DEC-2002;

27-DEC-2002;

27-DEC-2002;

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27-DEC-2002;
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Virag C,
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27-DEC-2002;
Sequence 1314 BP; 403 A; 214 C; 294 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-865361/80.
                                 invention
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B, Mansoury K,
Buzadzija K,
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2002US-0436345P
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2002US-0436676P
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2002US-0436734P
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Pinder B,
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Vallee F, Richards D,
Alam MZ, Tai M, Canad
 403 T; 0 U; 0 Other;
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                                    TTTCAAGTAACCATTCCTGATTTAAACTACCAGTATGAAGAGGGATATTTTGAGGAAGTT
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ds; UDP-N-acetylmuramoylalanine-D-glutamate ligase.
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                                                                                                                                                                                                                                                                                                  The invention relates to a composition (I) comprising purified polypeptides from bacteria. Also described: (1) a crystallized, recombinant polypeptide comprising an amino acid sequence of (I), where the polypeptide is in crystal form; (2) a crystallized complex comprising the crystallized, recombinant polypeptide and a co-factor or a small organic molecule, where the complex is in crystal form; and (3) a host cell comprising a nucleic acid encoding a polypeptide of (I), where a culture of the host cell produces at least about 1 mg of the polypeptide per liter of culture and the polypeptide is at least about one-third soluble as measured by gel electrophoresis. The composition and methods are useful for diagnosing, preventing or treating diseases, such as microbial infections. These may also be used in pharmacogenomic or drug screening procedures. The present sequence represents a Haemophilus influenzae UDP-N-acetylmuramoylalanine-D-glutamate ligase gene sequence, which is a composition of the polypeptide of the polypeptide of the polypeptide of the polypeptide is at least about one-third soluble as measured by gel electrophoresis. The composition and methods are useful for diagnosing, preventing or treating diseases, such as microbial infections. These may also be used in pharmacogenomic or drug screening procedures. The present sequence represents a Haemophilus which is a composition and methods and methods are useful for diagnosing procedures.
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Beattie
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Escherichia coli), useful for diagnosing, preventing or treating
microbial infections, or in pharmacogenomic or drug screening pro
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Ouyang H, I
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                                                                                   CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA
                                                                                                                     TAAACATTGAGCTAAATGCGTAAATTCTTCGCCGCGCTTTTCAAAAGAAGCAAACTGATC
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Pinder B,
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   TTTCAAGTAACCATTCCTGATTTÄAACTACCAGTÄTGÄAGAGGGATATTTTGAGGAAGTT
                              CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGCAGTT
                                                                     GTGCGGTTTGAATTTCTGGTGTTTTTACCGCAAGCCCTGGGCTAATAACAATCATATCGC
                                                                                                TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGG
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RESULT 10
ABE31251/c
ID AEB312
XX AEB312
XX AEB312
XX AEB312
XX O9-FEB
XX Vaccin
OS Haemop
XX NO-DEC
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PA (A
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               CC for the survival of Haemophilus sp. comprising a nucleotide sequence (C having at least 95% structural similarity with nucleotide sequence (C AEB31211, AEB31246 and AEB31027, AEB31140, AEB31145, C AEB31211, AEB31241, AEB31246 and AEB31231, and its complements, and (C AEB31211, AEB31241, AEB31246 and AEB31231, and its complements, and (C involves combining a polypeptide and an agent that binds a polypeptide, (C involves combining a polypeptide and an agent to form a mixture, where (C involves combining a polypeptide and an agent to form a mixture, where (C involves combining a polypeptide and an agent to form a mixture, where (C equence having at least 95% structural similarity with a nucleotide (C sequence chosen from AEB31062, AEB31130, AEB31140, AEB31155, AEB31311, AEB31246, AEB31263 and AEB31231, AEB311317, AEB31310, C AEB31241, AEB31246, AEB31263 and AEB31231, AEB31317, AEB31310, AEB313131, AEB31331, AEB31330, AEB31331, AEB31330, AEB31331, AEB31330, AEB31331, AEB31331, AEB31330, AEB31331, AEB31331, AEB31330, AEB31331, AEB31331, AEB31330, AEB31331, AEB31330, AEB3130, AEB31330, AEB313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      survival of Haemophilus sp. comprising an amino acid sequence having at least 95% structural similarity with an amino acid sequence chosen from AEE313117, AEE31330, AEE31332, AEE31335, AEE31354 and AEE313158. AEE31354 and AEE31358. Also described: (1) an isolated polynucleotide (II) critical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated polypeptide critical for survival of Haemophilus species, useful for reducing virulence of H. influenzae to be used as vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polypeptide (I) critical for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; SEQ ID NO 220; 158pp; English
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21-OCT-2002;
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) TREPOD C |
) ARVIDSON
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2002US-00274586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCACCATCATCAAATAAATAAAAATCTGC-CGTTTGGTGGCTAAGTAAGCTATTTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTTAAGGGTATCAAGCATGGCATCCATGGG
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TTGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCA
                                                             GGCGATAATCTTCTAAATCCATATAGCGATCCATATGATCTTCAGTCACGTTCAAGACAG
                                                                                                                 CCAAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGCGGAGAGATTTAAAATTG
                                                                                                                                                                              ---TATCTTCATTGTTCAACACACCTACTTTAGCATTATGATAAATGCGTAATTTTGCTT
                                                                                                                                                                                                                                                                                               CGCTTGATTTTCGTTTTCCCCAAAAGTCAGCC
                                                                                                                                                                                                                                                                                                                                                       TGATAATGGTGTGATTTGGGGCAACGCTTGTCAGTGTGGCTCAAGCATTGCTTGGCTAAAT 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACCAATGTAGCTTCTTCACAAGGTAAAATCACTTCATCTTTTACCATTAAATATTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATACCTATAGCTTGTGCCAATGCTGTTGCTGCCAAAATGTTCATATAATTATGGCGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGAAAACGATGATCTAACCCTTTGAAATGACGAAGTGCGGTACGAATTGAATCTAAATT 1788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAATGCAATTTACCCTCAATATA-----AAGCCCAGCCAATGCAGCAACTGTACT
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49.6%;
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AEE31130, AEE31140, AEE31155, AEE31211, AEE31241, AEE31246, AEE31263 and AEE31231, and determining if the H. influenzae comprising the mutation has reduced virulence compared to an H. influenzae that does not comprise the mutation; (5) an H. influenzae obtained by (M2); and (6) a vaccine composition comprising the H. influenzae. (1) is useful for reducing the virulence of H. influenzae to be used a vaccine composition, and for decreasing the growth rate of a microorganism. The present sequence represents a H. influenzae murb coding sequence, which is used in the
exemplification of the present invention.
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CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTT GAGACTTGCACAAGCAGCGACAATAATACCA-----TATCTCCGCTTTGCAA TAAACATTGAGCTAAATGCGTAAATTCTTCGCCGCGCTTTTCAAAAAGAAGCAAACTGATC TGTTGGGCGTAAAAATTCTATCGCTTGTTCCATTGTATCGAACAA----ATAACTTTG Score 160.4; 1 Pred. No. 3.7e. 0; Mismatches 1035 T; 0 U; 0 Other; DB 15; Indels Length 2925 , 88 Gaps 180 2133 2181 2079 120

1200 CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGCAGTT 1259	- VQ	ANANCTIACHUMACHAACANCHAINNIACH
103387 GTGCGGTTTGAATTTCTGGTGTTTTTACCGCAAGCCCTGGGCTAATAACAATCATATCGC 103328	Db	
1140 TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGG 1199	Q Y	61 CATGCTAGCACAAGCTGACAAAAGCACAGCCCTAGCGGTGCTTTTGACTGGCTGCTAA 120
103428GAĀTĀĀTĪCĀĀTĀĪCĪCĞĀTĀCTTCCĀCTCCCGCTTTAA 103388	Db	104439 TRAACATTGAGGTAAATTGGTAGAGTGGTTTTTTGAAAAGAACGAAATTGATC 1
1080 GTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTT 1139	Qγ	TAAACCTTTAGAACTTTAGAACTAGTTAACTAGTTAGAACTTTAGAAGTTTAGAAGTTTAGAAGTTGATGAACTTGATGAACTTGAGAGTTAGAAGTTGAGAGTTAGAAGTTGAGAGTTAGAAGTTGAGAGTTAGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTGAGTTAGAGAGTGAGAGTGAGAGTGAGAGTGAGAGTGAGAGTGAGAGTGAGAGAGTGA
TITTACCATTTGAACCTGTAATCCCCACAATTGGCTTTGTCGCTGCGCGGCA	Db 43	11.6%; Score 160.4; DB 2; Length 110000; ty 49.6%; Pred. No. 2.1e-34;
プレンエ ヤン・カン・カン・カン・カン・カン・カン・カン・カン・カン・カン・カン・カン・カン	÷	53_18 1800001
103540 CCATACCTARCTTTCACACCAGCAGCTTTCGCCATTTCATAAACTAAAGTAGTTACGGTAC 103481	Db	53_16 1600001 53_17 1700001
	γQ	WP AAT42063_14 1400001 1510000 WP AAT42063_15 1500001 1610000
103597 CATAAAGTTCACAATCTTCATTCAACAATGACAAAGCGGGAATCCCCAATATTTTCCGC 103541	Db	53_12 1200001 53_13 1300001
	γQ	53_10 53_11
103657 TCGCTGCCGCAGCTTTTAAGCTATAAGTTGTCTCCAAGCTGAAAACTAGAAAGCTCTAGTA 103598	B &	53_08 800001 900001
ערני איני איני איני איני איני איני איני א	Ş	53_06 600001
780 CCAMAINAICCHACHAIGHCHAINNEACHANNAILI HANNAILIG 833	B &	WP AAT42063_04 400001 510000 WP AAT42063_05 500001 610000
	P 5	200001
720 TIGGCATICGTCTTCGTTAGATGATGGCGGTTTGGCAATTTTCAAAAAATACGCAATTTTTTGTG // 9	ې کې	11 Name Begin End 13 00 1 110000
	t	plit into 19 fragments
	<u> </u>	(12 of 19) of ARTA2063 from base 1100001 (Wasmonbilis influenzac
660 TGATAATGGTGTGATTTGGGGCAACGCTTGTCAGTGTGGGTCAAGCATTGCTTGGCTAAAT 719	8	RESULT 11
GCCATTTTCAGTTTTTAGCCAATAATCCGCACTATTTTCCGCAAAAGAAACGGTATGTTT	당 .	Db 1008 AGÁGÁTÁAÍCCACÁCAAGAAÁGACCTÓTTTTGCCAÁGCCCGATGATAGTÁATATTTTT 951
	₹ ¦	QY 1320 CCAAAAAATTCACAGGCTGACAGTCCAGAGCTGCCCAAACCGACGACGGCATATTTTTT 1377
AACCAATGTAGCTTCTTCACAAGGTAAAATCACTTCATCTTTTACCATTAAATATTGCTT	da	Db 1068 TATCAATACCAGTAGGATTTTTTCGAGTATCAATCACGAATATTAGCCTGTTGGGATA 1009
TTTGATTTTTAATTGATGGATTGGTAAAAGTTTGTTTTTT	УО	0
103986 AATACCTATAGCTTGTGCCAATGCTGTTGCTGCCAAAATGTTCATATAATTATTGGCGACC 103927	D _D	Db 1128 TTTCAAGTAACCATTCCTGATTTAAACTACCAGTATGAAGAGGGATATTTTGAGGAAGTT 1069
	Qy	Qy 1200 CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGAACAATGAACGCCTGTGGGCAGTT 1259
	Db .	Db 1188 GTĠĊĠĠTTTGAÁTTTCTĠĠſĠŤŤTŤŤACCGCAÁGCĊĊTĠĠĠĊŤAÁŤAACAÁŤĊATÁŤĊĠC 1129
	Ov :	OY 1140 TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGGCTGATGATGATCTGATCCG 1199
351 GCGAGGIITGINGCIIIIGAALGAIIAANAIAIAGCEIIGCIA GAAIALGAIGAGGACTAA 104047	d dd	Db 1229GAATAATTCAATATCGCCGATTACTTCCACTCCGCTTTAA 1189
	? 5	QY 1080 GTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTT 1139
301 CANTOCCASTANTANOCCASTANAS ASCOCCASTONAS CONTRACTOR TO A 10/10/10/10/10/10/10/10/10/10/10/10/10/1	P &	Db 1281 TTTTACCATTTGAACCTGTAATCCCCACAATTGGCTTTGTCGCTGCGCGGCA 1230
		QY 1020 TITTGGCATTGAGCCTGTGATGGCGATGATTGGTGTGTTTGTT
241 CIGARIANCARINGCIGACAGOTICACIAAARITTIGACCITIKACAAGCCCACCAAAARI 300	F 9	Db 1341 CCATACCAACTTTCACACCAGCAGCTTTCGCCATTTCATAAACTAAAGTAGTTACGGTAC 1282
) b	Qy 960 CGACACCAACAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACAGTGC 1019
181 GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA 240	. Q	1398 CATAAAGTTCACAATCTTCATTCAACAATGACAAAGCGGGAATCCCCAATATTTCCGC
104331 TGTTGGGCGTAAAAATTCTATCGCTTGTTCCATTGTATCGAACAAATAACTTTG 104278	Db	900 CCACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGGCGTGCCAATATTACCGC 95
121 TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCCATCACCTTT 180	ΥQ	Db 1458 TCGCTGCCGCAGCTTTTAAGCTATAAGTTGTCTCAAGCTGAAAACTAGAAAGCTCTAGTA 1399

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RESULT 12

AAT42063 12/c

Continuation (13 of 19

WP Sequence split into

WP Sequence split into

WP AAT42063 00

WP AAT42063 01

WP AAT42063 03

WP AAT42063 03

WP AAT42063 06

WP AAT42063 07

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                 TTGAAAACGATGATCTAACCCTTTGAAATGACGAAGTGCGGTACGAATTGAATCTAAATT
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RESULT 13
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WP Sequence split into 3:
WP Fragment Name
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                TTGGCTAAATTGGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTTTCAAAAATACGC
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                 CTATCCACCCACTGCATAACATATGCTGACAGCTCACTAAAATCTTGACCTTTACCAAGC
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                                       al Similarity
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(29 of 34)
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                                                  157.6; DB 1
No. 1.4e-33;
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 05-MAR-2004;
                                                                                                  Haemophilus
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                                                                                                                                                     bacterial
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   2004WO-US007001
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                                                                                                                                                   infection; nasopharynx bacterial infection;
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Best Local Similarity
Matches 591; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises nucleotide sequences (genes) from the genome on nontypeable strain of Haemophilus influenzae (NTHi). The NTHI DNA sequences of the invention are useful for treating or preventing NTHi bacterial infections of the middle ear and/or nasopharynx. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides of nontypeable strain of Haemophilus influenzae, useful for treating or preventing NTHi bacterial infections of the mear and/or nasopharynx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14324 BP; 4572 A; 3171 C; 2271 G; 4310 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid represents an NTHi contig sequence of the invention.
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TAAAATTGTTGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAACTTGACAG
                                                    TTTTGCTTGGCGATAATCTTCTAAATCCATATAGCGATCCATATGATCTTCAGTCACGTT
                                                                                                                                                                                       GGTTTGTCTCGCTTGATTTTCACCTTCACCAAAAGTCAGC--------
                                                                                                                                                                                                                                                                                  ATGGCGACCGACTAATGTTACTTCTTCACAAGGCAAAATTACTTCATCTTTTACCATTAA
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                                                                                TTTTTGTGCCAAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGCGGAGAGATT
                                                                                                                                                   GGCTAAATTGGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTTTCAAAAATACGCAA
                                                                                                                                                                                                                    ATTTGTTGTGATAATGGTGATTTGGGGCAACGCTTGTCAGTGTGGTCAAGCATTGCTT
                                                                                                                                                                                                                                                        GTATTGCTTGCCATTTTCAGTTTTTAGCCAATAATCCGCACTATTTTCCGCAAAAGAAAC
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TTTTT 1377	GTGATTGACCAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGACGGCATA 1371 	GGGCAGTTTATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACC 1311	CTGATCGGCTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGT 1251	TTGAGCTTTGGCGGCGACAATACTCGGGGTTCTTGGGTTAATGCCGGGGCTGATGATGAT 1191	TAGATCTCGTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCC 1131	AACAGTGCTTTTGGCATTTGAGCCTGTGATGGCGATGATTGGTGTGTTTGTT	ATTACCGCCGACACCAACCATGCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGT 1011	CTCAAGCACCACAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGGCGTGCCAAT 951	CAAAACAGTCGCAGCCGCAGCTTTTAAGCTATAAGTTGTCTCAAGCTGAAAACTAGAAAG 5960

Search completed: May 18, 2006, 13:52:28 Job time: 955 secs

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GenCore version 5.1.8
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Title:
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1380
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12358.853 Million cell updates/sec
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RESULT 1 CZ543630/c

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 19	18	c 17	16	15	c 14	c 13	c 12	c 11	10	9	8	7	ი ი	ហ	C 4	u	ი 2	c 1	Result No.
47.6	48.6	49.4	49.8	50.2	52.6	54.2	55	56.8	59.6	62.2	69.8	76.4	77.2	80.2	80.8	92	92.8	98.2	Score
3.4	3.5	3.6	3.6	3.6	w	ω	4.0	4.1	4.3	4.5	5.1	5.5	5.6	5.8		6.7	6.7	7.1	Query
1101	958	452	572	838	1171	1024	474	628	928	623	1445	977	555	1025	916	892	709	817	Length DB
14	14	7	11	13	11	14	9	13	14	14	12	14	14	14	14	12	5	13	BB
CNSOOLOO	DU771470	BE184674	BH795426	CZ545153	BZ559806	DU732353	DR032465	CL691264	DU769542	AG952088	BZ568959	DU748329	AG943479	DU773354	DU735587	BZ579116	CF306940	CZ543630	ID
AL068607 Drosophi	DU771470 APKG2473	BE184674 PM4-HT068	BH795426 BMBAC376G		BZ559806 pacs2-164	DU732353 APKI1690.	DR032465 bda020270	CL691264 PRI0156a	DU769542 APKG1505.	AG952088 Drosophil	BZ568959 pacs2-164	DU748329 ASNC465.1	AG943479 Drosophil	DU773354 APKG3419.	DU735587 APKI3331.	BZ579116 msh2 6205	CF306940 HDA105-	CZ543630 SRAA-aad5	Description

45	44	43	42	41	40	39	c 38	37	c 36	c 35	c 34	ω u	32	31	c 30	c 29	c 28	c 27			c 24	C 23			c 20
41.4	41.4	41.6	41.6	41.6	41.8	41.8	42	42	42.2	42.2	42.4	42.4	42.8	43	43.6	44	44.4	44.4	44.4	45	45	45	45.4	46	47.2
3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3. ₁	3.1 1	3. ₁	3. ₁	ω ,	3.1	3.2	3.2	3.2		3.2	ω .ω	ω .ω	ω .ω	ω ω	3.3	3.4
760	639	747	714	616	1101	517	1022	941	915	747	1101	934	1101	1035	692	918	794	490	442	907	757	590	856	823	1101
11	9	4.	11	11	14	-ب	14	14	11	13	14	14	14	14	11	14	10	œ	10	φ	10	_	14	10	14
BH367641	CX639436	CA920035	BH374901	BH383040	CNS000D1	AU287702	CNS07ANB	CNS05L54	AZ543308	CZ668937	CNS0039G	DU791861	CNS0100X	CNS00ZD5	BH983612	DU772406	DR473810	CO253110	DR565020	DN922769	DR473894	AU287701	AJ863943	DR505933	CNSOOZMK
BH367641 AG-ND-127	CX639436 UCRPT02_4	CA920035 EST637753	BH374901 AG-ND-127	BH383040 AG-ND-127	AL065414 Drosophil	AU287702 AU287702	AL436797 T3 end of	AL342337 Tetraodon	AZ543308 ENTGK93TR	CZ668937 OM_Ba022	AL063921 Drosophil	DU791861 APKH4300.	AL098379 Drosophil	AL097523 Drosophil	BH983612 ode20g11.	DU772406 APKG2941.	DR473810 WS00960.B	CO253110 WS00818.B	DR565020 WS02632.C	DN922769 43863.2 C	DR473894 WS00960.B	AU287701 AU287701	AJ863943 Ralstonia	DR505933 WS02715.B	AL097862 Drosophil

JOURNAL COMMENT REFERENCE AUTHORS ACCESSION VERSION KEYWORDS FEATURES SOURCE ORGANISM DEFINITION Snoo TITLE source GSS; Strongyloides ratti Strongyloides ratti Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Eukaryota; Metazoa; Strongyloididae; Strongyloides. 1 (bases 1 to 817) Mitreva,M., McCarter,J.P., Thompson,F., Viney,M., Pape,D., Ritter,E., Martin,J., Wylie,T., Dante,M., Waterston,R.H., Clifton,S.W. and Wilson,R. Genome Survey sequences from the rat parasitic nematode Strongyloides ratti Washington University in St. Louis Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Unpublished (2005) Contact: Mitreva M CZ543630 817 bp DNA linear GSS 13-MAY-2005 SRAAA-aad51b03.gl Strongyloides ratti whole genome shotgun library (SRAAGSS 004) Strongyloides ratti genomic, genomic survey sequence. CZ543630 Class: shotgun. Email: nematode@watson.wustl.edu Genomic DNA was provided by Fiona Thompson (F.Thompson@bristol.ac.uk) and Mark Viney (Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol, Tel: 314 286 1800 Fax: 314 286 1810 CZ543630.1 GI:64673383 /organism="Strongyloides ratti" /mol_type="genomic DNA" /strain="Isofemale line ED321 heterogonic" /db_xref="taxon:34506" /dev_stage="infective larval stage (iL3)" /lab_host="GS10" Location/Qualifiers note="Vector: pOTW13; Site_1: BstX1; Site_2: BstX1; clone_lib="Strongyloides ratti whole genome shotgun ibrary (SRAAGSS 004)" . 817 Louis, MO 63108, USA

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RESULT 2
CF306940/c
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                                                                                                                                                                                                                            Genomics and Genetics Institute, GreenGene Biotech Inc.; of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
                                                                                                                                                                                                                                                                                                                                                                      Large-scale Sequencing Analysis 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                         Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clade; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                    bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
Location/Qualifiers
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/tissue_type="callus"
/dev_stage="proliferated
                                                                  /organism="Oryza sativa
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
                                             clone="HDA1--05-E12"
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Pred. No. 1.5e-16;
0; Mismatches 138;
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                                                                                                                                                                                      Tel: 2062216954
Fax: 2066857244
                                                                                                                                                                                                                          University of Washington
Box 352145, Seattle, WA 98105-2145,
                                                                                                                                                                                                                                                                                J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                 Whole-Genome-Sequence variation among multiple Psedomonas aeruginosa library
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BZ579116.1 GI:27214177
                                                                                                                                                   Class: shotgun.
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/db_xref="taxon:287"
/clone="msh2_6205"
/clone_lib="msh"
                                                       /mol_type="genomic
/strain="MSH"
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Pred. No. 5.3e-15;
0; Mismatches 142;
                                                                            DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp DNA linear GS aeruginosa genomic clone
                                                                                            aeruginosa'
                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                        Sime, E
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                                                                                                                                                                                                                                                                                                                                                                        Hastings, M.
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/note="Environmental isolate. Whole genomic shotgun

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RESULT 4
DU735587/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 GTGGTAGTCAGCCATGCCGTCGTAGCGATCCATATGGTCTTCGCTGACGTTCAGCACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   721 GGCATCGTCTTGGTAGATGACGGCGGTTTGGCAATTTTCAAAAATACGCAATTTTTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           916 bp DNA linear GSS 27 APKI3331.g2 HF70_10-07-02 uncultured marine microorganism HF70_10-07-02 genomic clone HF0070_040C09. Genomic DU735587
                                                                                                                                                                                                   Email: PMRichardson@lbl.gov; delong@mit.edu
Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth 70
Temperature: 24.93 C Salinity: 35.21 psu Oxygen: 217.4 umol/
                                                                                                                                                                                                                                                                                                   US DOE Joint Genome Institute
US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut Creek,
                                                                                                                                                                                                                                                                                                                                                          Science (2006) In press
Contact: Susan Lucas, Alex Copeland,
Kerrie Barry, Tijana Glavinadelrio, I
and Edward DeLong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frigaard, N.U., Martinez, A., and Karl, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uncultured marine microorganism HF70_10-07-02 uncultured marine microorganism HF70_10-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DeLong, E.F., Preston, C.M., Mincer, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unclassified sequences; environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGGCGTGCCAATATTACCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAPATRATCCACCATGCCATCGTGCCGATCAAGATGATCAGCGGAGAGATTTAAAATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACACCAACAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACAGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 916)
                                                                                                                                                                                                                                                                617-253-2679
                                                                                                                                                                                        fosmid ends
/mol_type="genomic DNA"
/db_xref="taxon:361144"
/dlone="HF0070 040C09"
/clone="HF0070 040C09"
/clone lib="HF70 10-07-02"
/note="Vector: pCC1FOS; North Paci
                                                                                                                                                                      Location/Qualifiers
                                                                                                                                 organism="uncultured marine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.7%;
56.3%;
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Pred. No. 9.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                               in the ocean's interior
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ecological trends
                                                                                                                                                                                                                                                                                                                                                                            David Bruce, I
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                                                                                                                                 microorganism
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   Pacific Subtropical Gyre
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                                                          um,
                                                        greater
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SOURCE
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Best Local S
Matches 185
                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1018 GCTTTTGGCATTTGAGCCTGTGATGGCGATGATTGGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              718 ATTGGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTTTCAAAAAATACGCAATTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 ACTITTGCCATTGGTTCCAGTGATCGCCATCACCGATGCG
                                                                                                                                                                US DOE Joint Genome Institute
US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut
Tel: 617-253-5271
Fax: 617-253-2679
                Email: PMRichardson@lbl.gov; delong@mit.edu
North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fo
DNA library prepared from marine picoplankton in the less than
um, greater than 0.22 um fraction. Sample Date: 12/21/2003
Coordinates: 22.45 N, 158 W Depth 4000 m Temperature: 1.46 C
Salinity: 34.69 Oxygen: 147.8 umol/kg
Class: fosmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                           1 (Dases 1 to 1025)
1 (Dases 1 to 1025)
DeLong, E.F., Preston, C.M., Mincer, T., Ric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DU773354 1025 bp DNA linear GSS 27 APKG3419.g2 HF4000_12-21-03 uncultured marine microorganis HF4000_12-21-03 genomic clone HF4000_[384]008F16, genomic
                                                                                                                                                                                                                                                                               Science (2006) In press
Contact: Susan Lucas, Alex Copeland,
Kerrie Barry, Tijana Glavinadelrio,
and Edward DeLong
                                                                                                                                                                                                                                                                                                                                                                  Comparative genomics reveals ecological trends microbial communities in the ocean's interior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uncultured marine microorganism HF4000_12-21-03 uncultured marine microorganism HF4000_12-21-03
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GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                Frigaard, N.U., Martinez, A., and Karl, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unclassified sequences; environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGGCCACATCAGAACGAAACGCACCTGCACTTTCAAGTTGGTAACTGGAAATCTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCCAAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGCGGAGAGATTTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAGTCAGTTTCTTTGATTGACCACTGCGATGTTTGTACGCCGGTACAATGACGCTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCCACTTTCATGGACATAGCAGCATCTCCGCCATCTGACCCAGTAATGTCGTTACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGGCGTGCCAATATTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCGTAGTAGTGCTCCAGGTTGTCGTAGCGATCAAGATGATCCGGCGCAAGGTTGAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Hawaii) picoplankton genomic fosmid DNA library prepared from marine picoplankton in the less than 1.6 um, greater than 0.22 um fraction. Picoplankton collected at 70 m depth on 10/7/2002, Coordinates: 22.45 N, 158 W Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth 70 m Temperature: 24.93 C Salinity: 35.21 psu Oxygen: 217.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.4%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.8; DB 14;
No. 1.7e-11;
                                                                                                                                                                                                                   Creek,
                                                                                                                                                                                                                                                                                                      David
                                                                                                                                                                                                                                                                                                        Sam Pitluck,
David Bruce,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Rich,V., Hallam,S.J.,
M., Edwards,R., Chisholm,S.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      marine microorganism
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                                                                                                                                                                                                                     94598-1698,
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                                                                                                                                                                                                                                                                                                        Paul Richardson
                                                                                                                                                                                                                                                                                                                               Alla Lapidus,
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
AG943479/c
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                                                                                                                                                                                                                                                                                                                       sequence.
AG943479
AG943479.1
Submitted (19-JAN-2005) Masahira Hattori, The Institute of Phyand Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                 Drosophila ananassae
Drosophila ananassae
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta,
Neoptera, Endopterygota, Diptera, Brachycera, Musco
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                  Hattori, M.
                                                                                                                                BAC end sequences of Library Unpublished
                                                                                                                                                   Hattori,M., Toyoda,A.,
Toshio,T.K. and Sakaki,
BAC end sequences of Li
                                                                                                                                                                                                                                                                                                                                                                        AG943479
Drosophila ananassae
                                                                                    Direct Submission
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                                                                                                                  (bases 1 to 555)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="HF4000_12-21-03"
/note="Vector: pCCIFOS; North Pacific Subtropical Gyre
/note="Vector: pCCIFOS; North Pacific Subtropical Gyre
(Hawaii) picoplankton genomic fosmid DNA library prepared
from marine picoplankton in the less than 1.6 um, greater
than 0.2 um fraction. Picoplankton collected at 4000 m
depth on 10/7/2002, Coordinates: 22.45 N,158 W Sample
Date: 12/21/2003 Coordinates: 22.45 N, 158 W Depth 4000 m
Temperature: 1.46 C Salinity: 34.69 Oxygen: 147.8 umol/kg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/db xref="taxon:361148"
/clone="HP4000 [384]008F16"
/cell type="marine picoplankton,
than 0 22 um fraction"
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HF4000_12-21-03"
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Pred. No. 2.6e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163;
uncultured marine microorganism HF10_10-07-02 uncultured marine microorganism HF10_10-07-02 unclassified sequences; environmental samples. 1 (bases 1 to 977)

DeLong, E.F., Preston, C.M., Mincer, T., Rich, V., Frigaard, N.U., Martinez, A., Sullivan, M., Edward and Karl, D.M.

Comparative genomics reveals ecological trends microbial communities in the ocean's interior
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Saga Ippongi-cho, Ukyo-ku, Kyoto 616-83
Tel: 81-75-873-2660 FAX: 81-75-861-0881
                                                                                                                                                                                                        DU748329.1
GSS.
                                                                                                                                                                                                                                                                  DU748329 977 bp DNA linear GSS:
ASNC465.b2 HF10_10-07-02 uncultured marine microorganism
HF10_10-07-02 genomic clone HF0010_001A11, genomic surve
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LIBRARY
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1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa
(E-mail:hattoriégsec.riken.jp,Tel:81-45-503-9111,
Fax:81-45-503-9170)
                                                                                                                                                                                                                                               DU748329
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Submitted (30-11-2004) by Masahira Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clones are derived from the BAC library DNB1
For BAC library availability, please contact Masa-Toshi Yamamoto
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/mol type="genomic DNA"
/db xref="caxon:7217"
/clone="DNB1-017M23.R.fa"
/clone_lib="DNB1 Drosophila
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Pred. No. 1.6e-10;
0; Mismatches 143;
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l.6e-10;
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                                                                       Rich, V., Halla
M., Edwards, R.,
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ds.R., Chisholm,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science (2006) In press Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus, Kerrie Barry, Tijana Glavinadelrio, David Bruce, Paul Richardson and Edward DeLong US DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fo DNA library prepared from marine picoplankton in the less than um, greater than 0.22 um fraction. Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth: 10 m Temperature: 26.4 C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: PMRichardson@lbl.gov; delong@mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 617-253-5271
Fax: 617-253-2679
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TCAGCGGAGAGATTTAAAATTGTTGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGC
                                                                                                                                                                                                                                                                                                                             GCATTGAGTAGGTTATGCTTTGCTTTTGATTTTAATTGATGGATTGGTAAAAGTTTTGTTT
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                                                 TGGTAAATCCTCTGCTTTATGCGCTGATAATTGTCCATGCTGTGATGACGATCTAAATGA
                                                                               TCAAAAATACGCAATTTTTGTGCCAAATAATCCACCATGCCATCGTGCCGATCAAGATGA
                                                                                                                GTGTCCAAGGGCTTAGTTAA----GGGATCATGGCGATTAAAAATGATAGATTCTGCGCCT
                                                                                                                                             GTCAAGCATTGCTTGGCTAAATTGGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTT
                                                                                                                                                                            GGTTGATCAATACCAAAACTTTTCAGACTAG
                                                                                                                                                                                                            TGGCTAAGTAAGCTATTTGTTGTGATAATGGTGTGATTTTGGGGCCAACGCTTGTCAGTGTG
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/clone_lib="HFI0_10-07-02"
/note="Vector: pCC1FOS; North Pacific Subtropical Gyre /Housil picoplankton genomic fosmid DNA library prepared from marine picoplankton in the less than 1.6 um, greater than 0.22 um fraction. Picoplankton collected at 10 m depth on 10/7/2002, Coordinates: 22.45 N, 158 W. Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth: 10 m Temperature: 26.4 C Salinity 35.08 psu Oxygen: 204.6
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Pred. No. 3.2e-10;
0; Mismatches 256
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Box 352145, Seattle, WA
   AG952088
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ilarity 55.0%;
Conservative
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pacs2-164_8171, genomic survey sequence.
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/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole
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|mol_type="genomic DNA"
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Best Local Similarity
Matches 176; Conserv
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-JAN-2005) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the BAC library DSE1 For BAC library availability, please contact Masa-Toshi Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila sechellia
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (yamamoto@kit.jp).
Submitted (30-11-2004) by Masahira Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila sechellia DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetic Resource Center
Saga Ippongi-cho, Ukyo-ku, Kyoto 616-8354, Japan
Tel: 81-75-873-2660 FAX: 81-75-861-0881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN, Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa
[E-mail:hattori@ggc.riken.jp,Tel:81-45-503-9111,
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                                      CGTGCCAATATTACCGCCGACAACCAACCATGCCTGCATGTTTTGCCATCTCGCCTAC 1002
                                                                          AGAGGAGAGTTCGATTACATAAATTTCTGCATCTC-----TTTCTAGATCCAAAACAGG
                                                                                                              ACTTGACAGCTCAAGCACCACCAAATCCATATTTTGGATCGTTAATAATTCAAGTGCAGG
                                                                                                                                                      AATACGCAATTTTTGTGCCAAATAATCCACCATGCCATCGTGCCGATCAAGATGATCAGC 822
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R.Site 2
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/db_xref="taxon:7238"
/clone="DSE1-004A05.F.fa"
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/clone_lib="DSE1 Drosophila
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Pred. No. 3.7e-06;
D; Mismatches 163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: PMRichardson@lbl.gov; delong@mit.edu
North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
DNA library prepared from marine picoplankton in the less than 1.6
UM, greater than 0.22 um fraction. Sample Date: 12/21/2003
Coordinates: 22.45 N, 158 W Depth 4000 m Temperature: 1.46 C
Salinity: 34.69 Oxygen: 147.8 umol/kg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US DOE Joint Genome Institute
US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut Creek,
Tel: 617-253-5271
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Kerrie Barry, Tijana Glavinadelrio, David Bruce, Paul Richardson
and Edward DeLong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science (2006) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microbial communities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uncultured marine microorganism HF4000_12-21-03 uncultured marine microorganism HF4000_12-21-03 unclassified sequences; environmental samples.
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TGAAAACTTGACAGCTCAAGCACCACCAAATCCATATTTTGGATCGTTAATAATTCAAGT
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/note="Vector: pCCIFOS; North Pacific Subtropical Gyre
/note="Vector: pCCIFOS; North Pacific Subtropical Gyre
(Hawaii) picoplankton genomic fosmid DNA library prepared
from marine picoplankton in the less than 1.6 um, greater
than 0.22 um fraction. Picoplankton collected at 4000 m
depth on 10/7/2002, Coordinates: 22.45 N,158 W. Sample
Date: 12/21/2003 Coordinates: 22.45 N, 158 W Depth 4000 m
Temperature: 1.46 C Salinity: 34.69 Oxygen: 147.8 umol/kg"
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/db xref="taxon:361148"
/clone="HF4000 [384]003B18"
/cell type="marine picoplankton,
than 0.22 um fraction"
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                                                                434 AAGGCTGGCACAGGCTGGGGAGGAGCAGAACCAT
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                                                                                                                                                                                                     61 CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
Seq primer: T7
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
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Pristionchus pacificus
Eukaryota, Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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AACACGCGGAGCCAAGCGCATCGCCTGTTCCATAGTTTCGGTTTGTTCTGCCACTTC
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Location/Qualifiers
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/mol_type="genomic DNA"
/strain="California"
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one lib="Mixed stage fosmid library of P.
California"
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                                                                                                                                                                                                                                                                                                       Score 56.8; DB 13;
Pred. No. 0.00014;
0; Mismatches 242;
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                               1231 AAAATGACAATGAACGCCTGTGGGCAGTTTATCTGCCAAGGTAGGATTGGGATTACCATC
                                                                                                 1171 AATGCCGGGGCTGATGATGATCTGATCGGCTGAGCTTAAGAGTTCACTGTCCAAGCTGCC 1230
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bda020270D15.ab1_061 Antrodia ccinnamomea cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO.1, Section 4, Roosevelt Road,
Tel: 886 2 3366 4595
Fax: 886 2 2362 0639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypora causing b
Unpublished (2005)
Contact: Tzean SS
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                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: 5' GTAAAACGACGGCCAGT 3'
BACKWARD: 5' CACACAGGAAACAGCTATGACCAT 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: sst@ntu.edu.tw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Plant Pathology and Microbiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Analysis of expressed sequence tags from Antrodia cinnamomea, polypora causing brown rot of Cinnamomum kanehirai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Aphyllophorales; Antrodia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antrodia cinnamomea
Antrodia cinnamomea
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EST.
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CGTGTGGCGTTCTACGGCTTCGGGTAATTTATCCAGGCCAGGCGGTGTCATACGCGTATC
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                                                                  AATACCGGGACTGGCGACAATCAGATCTGCCGCCATCAGCCATTCATCATTCAGACTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1
                                                                                                                                 Conservative
                                                                                                                                                                                                             /lab_host="Cinnamomum kanehirai"
/clone_lib="Antrodia cinnamomea cDNA Library"
/note="Yector: ZAP Express Vector"
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                 db_xref="taxon:279009"
                                                                                                                                                                                                                                                                                                                                mol_type="mRNA"
                                                                                                                                                                                                                                                                                sex="Heterokaryon"
                                                                                                                                                                                                                                                                                                                  strain="SMV 1"
                                                                                                                                                                                                                                                                                                                                                organism="Antrodia
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a cinnamomea
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                                                                                                                                                                                                                                                Local
                                                                            497
437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: PMRichardson@lbl.gov; delong@mit.edu
Sample Date: 10/7/2002 Coordinates: 22.45 N, 158
Temperature: 24.93 C Salinity: 35.21 psu Oxygen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1024)
DeLong, E.F., Preston, C.M., Mincer, T., Rich, V., Hallam, Prigaard, N.U., Martinez, A., Sullivan, M., Edwards, R., Card Free Company (N. 10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uncultured marine microorganism HF70_10-07-02 uncultured marine microorganism HF70_10-07-02 unclassified sequences; environmental samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DU732353 1024 bp DNA linear GSS 27APKI1690.b2 HF70_10-07-02 uncultured marine microorganism HF70_10-07-02 genomic clone HF0070_025B08, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US DOE Joint Genome Institute
US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut Creek,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kerrie Barry, Tijana Glavinadelrio, and Edward DeLong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science (2006) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microbial communities in the ocean's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: fosmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Susan Lucas, Alex Copeland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Comparative genomics reveals ecological trends in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Karl, D.M.
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                                                                                                                                                                                                                                                  Similarity
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                                                                            AGCGCACGCCCTTGACTTGACTGATTAGCTGGCAGCGATGGGGCAGACCTCGGCACTGCT
                                                                                                         ATGCCTTGCTATCAATATCATCAATATATTCACAGCGATGCGGTAGCCCCTTTGAAAGTCT
                                                                                                                                                       CCAGGCCCTCCAGCGCGGCCGCCGTCGCACCGATATTGGTGCCTTTTGCTGTCATCGATGA 498
                                                                                                                                                                                        CAAGCCCATCAATTGCTGCAATGGTTGAGCCGATGTTTGTACCTTTTGAATCATTAAAAT 392
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                                    TAAGGGTATCAAGCATGGCATCCATGGGAAGATTGGCAGCTGTGCCTAAGGCAAGTGCAG
  TTGCTCCCTCGATCAGTCCCTCGAGGGGCATTTTCAACGCGCTGCCCAGTGACAACGCCG
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                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="HF70_10-07-02"
/note="Vector: pCCLFOS; North Pacific Subtropical Gyre
/note="Vector: pCCLFOS; North Pacific Subtropical Gyre
(Hawaii) picoplankton genomic fosmid DNA library prepared
from marine picoplankton in the less than 1.6 um, greater
than 0.22 um fraction. Picoplankton collected at 70 m
                                                                                                                                                                                                                                                                                                                                               depth on 10/7/2002, Coordinates: 22.45 N, 158 W Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth 70 m Temperature: 24.93 C Salinity: 35.21 psu Oxygen: 217.4
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                                                                                                                                                                                                                                                                                                                                 umol/kg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:361144"
/clone="HF0070_025B08"
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                                                                                                                                                                                                                                                  3.98;
                                                                                                                                                                                                                                Score 54.2; DB 14;
Pred. No. 0.00088;
0; Mismatches 118;
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217.4 umol/kg
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Paul Richardson
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Chisholm,
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pacs2-164 1863, genomic survey sequence.
BZ559806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1171)
Spencer, D.H., Raymond, C.K., Smith, E.E.,
Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Washington Box 352145, Seattle, WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonadaceae; Pseudomonas.
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                                        TATATTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGGGTATCAAGCATGGCATCCA
                                                                                                                   CGGCGCCGACGTTGGTGGCCTTGGAATCGTCGTAGTAGCTCACGCCCTGCCGCTCGCGTA
                                                                                                                                                       TTGAGCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATCAA
                                                                                                                                                                                              CGATCAGCACCAG----CTTGCCGTCGATGTCGGCACCCAGCCCTCGATCGCCGCCAGGG
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  TGGGAAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db xref="taxon:287"
/clone="pacs2-164 1863"
/clone_lib="pacs2-164"
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0; Mismatches 174;
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                                                                                                                             1006 TGTCGTAACAGTGCTTTTGGCATTTGAGCCTGTGATGGCGATGATTGGTGTTTTGTTGC 1065
                                         1066 TTGAGTT 1072
                                                                                  136 AGACGTTGTCGTTGTTTTTCCGTTGCTTCCTGTGATCGCAATGATTTTCGCATCGGTAAA 195
196
                                                                                                                                                                                                946 GCCAATATTACCGCCGACACCAACCATCCATGCCTGCATGTTTTGCCATCTCGCCTACTAA 1005
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                                                                                                                                                                                                                                                           79;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Strongyloides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Survey sequences from the rat parasitic nematode strongyloides ratti Unpublished (2005) Contact: Mitreva M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CZ545153 838 bp DNA
SRAA-aad60c01.g1 Strongyloides ratti whole
(SRAAGSS 004) Strongyloides ratti genomic,
CZ545153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 838)
Mitreva,M., McCarter,J.P., Thompson,F., Viney,M., Pape,D.,
Ritter,E., Martin,J., Wylie,T., Dante,M., Waterston,R.H.,
Clifton,S.W. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UK.
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: nematode@watson.wustl.edu
Genomic DNA was provided by Fiona Thompson
(F.Thompson@bristcl.ac.uk) and Mark Viney
(Mark.Viney@bristcl.ac.uk) at the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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Similarity 62.2%;
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TTCAGAT 202
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pOTW13; Site_1: BstX1; Site_2: BstX1; Strongyloides ratti genomic DNA was randomly sheared, end-repaired and size fractioned to enrich for 2-4 kb fragments. Genomic DNA was provided by Fiona Thompson (F.Thompsonabristol.ac.uk) and Mark Viney (Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol, UK. Sequencing by Washington University Genome Sequencing Center, St. Louis, MO."
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library (SRAAGSS 004)"
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genome shotgun library
genomic survey sequence
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Search completed: May 18, 2006, 11:52:44

Job time : 6248 secs

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1: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/P_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/P_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/AE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*
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ACAAGCAC ACAAGCAC ATCAAGTC ATCAAGTC ATCAAGTC	100.0 y 100.0 rvative GAACCATGT [8 1352 5 U 6 536 3 U 7 6 699 3 U 7 6 1320 3 U 7 1348 3 U 7 134 3 U 7 1350 2 U 7 135
CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCCTAGCTAG	100.0%; Score 1380; DB 3; imilarity 100.0%; Pred. No. 0; ; Conservative 0; Mismatches 0; TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTC	US-09-974-300 US-09-147-928 US-09-114-000 US-08-956-1711 US-08-956-1711 US-08-956-1711 US-09-9710-279 US-09-9710-279 US-09-9734-001 US-09-902-540 US-09-901-527 US-09-961-527 US-09-961-527 US-09-9665-4355 US-08-665-4355 US-08-665-4355 US-08-665-4355 US-08-665-4355 US-08-665-4355 US-08-843-309 US-08-843-309 US-08-9583-110 US-08-9583-110 US-08-9583-110 US-08-9583-110 US-08-9583-110 US-08-9583-110
AAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA	DB 3; Length 96109; 0; Indels 0; Gaps ICGCTCATTATAATTTTAAATTGATC ICGCTCATTATAATTTTTAAATTGATC	XELLA C
ACTGGCTGCCAA 120	96109; 0; Gaps 0; TTAAATTGATC 60 	Sequence 1685, Apsequence 3, Appli Sequence 80, Appli Sequence 80, Appli Sequence 80, Appli Sequence 1001, Appli Sequence 155, Appli Sequence 173, Appli Sequence 175, Appli Sequence 197, Appli Sequence 22, Appli Sequence 3, Appli Sequence 1, Appli Sequence 3, Appli Sequence 1, Appli Sequence 197, Appli Sequence 197

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                                                                          TGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGCAGTTT
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RESULT 2
US-09-540-236-7734c
; Sequence 673, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OR INVENTION: NUMBER CACID AND AMINO A TITLE OF NAVENTION: FULGROSTICS AND THER FILE REFERENCE: 2709-2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 673
; LENGTH: 1410
; ORGANISM: M.catarrhalis
US-09-540-236-673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 1374; Conserv
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CAATGCCAGTGATGATATGCCATAAACCGTGCCAAGCCCATCAATTGCTGCAATGGTTGA 360
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ilarity 99.6%;
Conservative
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US-09-328-352-1282/c Sequence 1282, Application US/09328352 Patent No. 6562958 GENERAL INFORMATION: APPLICANT: Gary L. Breton et al. TITIE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITIE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITIE OF INVENTION: NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 SEQ ID NO 1282 SEQ ID NO 1282 SEQ ID NOS: 8252 SE	Qy 1321 CAAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGACGACTATTTTTTGA 1380	OY 1201 TGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGAACAATGAACGCCTGTGGGCAGTTT 1260	1081 TGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTTT	Oy 961 GACACCAACAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACAGTGCT 1020	Oy 721 GGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTTTCAAAAATACGCAATTTTTTGTGC 780
OY 776 TGTGCCAAATAATCCACCATGCATCAAGATGATGATGATATACAACTTTAAAAAATACCAATGATGATTTAAA 835	Db 766 TİAAACCAÀÁGCTTTGCÁTTGĞTĞTĞGĞTATCTĞĞAACAAĞTĞĞACĞGCTTA 716 Qy 716 AAATTGGCATCGTCTTGGTAGATGATGGCGGTTTTGGCAATTTTCAAAAATACGCAATTTT 775	Db 878 AÏACCITGAATATATAAATCTGAGCTTTAATTAACCGCTGTAAACCACGAGCAAGCCAA 819 Qy 596 ATACCATCACCATCACTAATAAATAAAATCTGCCGTTGGTGGCTAAGTAAG	UR VO 45 VO	Db 1118 AGTGCAACCTTACCTTTTTTCACTTCAATGGCAGCCTAAGCCATCAATTGCTGCAAGT 1059 Oy 356 GTTGAGCCGATGTTTGTACCTTTTGAATCATTAAAATTATGCCTTCAATATCATCA 415	Db 1349 AAACTTGCCCGATCAAGTGTATCCAACCTGATATTTTAGATGCCAAATGTGCACATCTTCAC 1298 Qy 122 ACTGCCCGATCAAGTGTACCAACCTGATATTTTTAGATGCCAAATGTGCATCATCATCTTCAC 1298 Db 1297 GTTGACAAGCTTGAACGTTCTTTAAGCGTTGCTGCAAATTTTAGTTGCGCCT- 1239 Qy 182 AGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCAC

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1203387 GTGCGGTTTGAATTTCTG	CTAGCGGTGCTTTGACTGGCTGCCAA 120	61
1140 TGGCGGCGACAATACTCGG	TARACATTGAGCTARATGCGTARATTCTTCGCCGCGCTTTTCARARGARGCARACTGATC 1204380	Db 1204439 TAAACATTG
1203428	AACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC 60	Qy 1 TAAAGCGTC
	11.6%; Score 160.4; DB 3; Length 1830121; larity 49.6%; Pred. No. 9.6e-37; Conservative 0; Mismatches 606; Indels 89; Gaps 7;	Query Match Best Local Similarity Matches 683; Conser
1020 TTTTGGCATTTGAGCCTG		
1203540 CCATACCAACTTTCACAC	DESCRIPTION: SEQ ID NO: 1:	TOPO
1203597 CATAAAGTTCACAATCTT	palrs	; LENGTH: 1
	•	INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
1203657 TCGCTGCCGCAGCTTTTA	TELEPHONE: 301-309-8504 Db TELEPAX: 301-309-8439	TELEPHONE TELEPHONE TELEFAX:
840 TIGCCCCTIGAGCIGCCA	REGISTRATION NUMBER: 41,971 REFERENCE/DOCKET NUMBER: PB186P3 TELECOMMUNICATION TURODMATION QY	REGISTRAT
1203717 GGCGATAATCTTCTAAAT	INFORMATION: Db	; ATTORNEY/AGENT
780 ссладтадтссассатес	APPLICATION NUMBER: 08/4/6,102 FILING DATE: JUN-5-1995 QY	; APPLICATI
1203774TATCTTCATTGTTCA	ION TOTAL: Db	; PRIOR APPLICAT
720 TGGCATCGTCTTGGTAGA	FILING DATE: 25-ABR-2000 CINCIETTATION THE CONTROL OF T	FILING DA
1203806 CGCTTGATTTTCGTTTTC	NT APPLICATION DATA: Db ABBLICATION NTABER. 116/00/557 08/	CURRENT APPLIC
660 TGATAATGGTGTGATTTG	SYSTEM: MS DOS v6.22 Qy	OPERATING
1203866 GCCATTTTCAGTTTTTAG	MEDIUM TYPE: 3 1/2 inch diskette	COMPUTER READABLE MEDIUM TYPE:
601 ATCACCATCATCAATAA		; COUNTRY: U
1203926 AACCAATGTAGCTTCTTC	ROCKVILLE Db	; CITY: ROC.
541 TTTGATTTTTAATTGATG	Human Genome Sciences, Inc. 410 Key West Avenue Qy	ADDRESSEE: HO STREET: 9410
1203986 AATACCTATAGCTTGTGC		; NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
481 AAGATTGGCAĢÇTGTGCÇ	Haemophilus reof, and Us	**
	APPLICANT: Fleischmann et al. TITLE OF INVENTION: The Nucleotide sequence of Db	APPLICANT: Fle
1204100 CCCCACAIIIGIIGCIIII	11 40/0333/004	; Patent No. 6506581 ; Patent No. 6506581
		RESULT 4 US-09-557-884-1/c
1204157 CAÑATGCÁATTTACCCTC	Db	
301 CAATGCCAGTGATGATATV	TCATGCAGGAAATTTACAGCAGAAACACCTGATATTCCCAAAGCCTGCTACAACTTTT 93	Db 149 TCATGCAGG
	PGT 150	209
241 CTGCATAACATATGCTGA	AGTTTATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGA 1315	Qy 1256 AGTTTATCT
181 GAGTAAATCTTGCTCAAT	TCTGCTTGTAATAATTCTTGATCAAGCTGACCAAAACTGGTTTTAACACCAGCCGGA 210 Ph	Db 269 TCTGCTTGT
1204331 TGTTGGGCGTAAAATTC	TCGGCTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGC 1255	
	GCAATAGCTGCCTGAATTTCCGGTAATTGTGGTGCAAGGCCTGGGCCTTAAAATAATCTCT 270	Db 329 GCAATAGCT

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CAATATA-----AAGCCCAGCCAATGCAGCAACTGTACT 1204107
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                                                                                                                                                                                                                                                                                        ATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTT 1139
                                                                                                                                                                                                                                                                                                                                                                  GTAATCCCCACAATTGGCTTTGTCGCTGCGCGCA----- 1203429
                                                                                                                                                                                                                                                                                                                                                                                                                           GTGATGGCGATGATTGGTGTTTGTTGCTTGAGTTAGATCTC 1079
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                                                                                                       GTGTTTTTACCGCAAGCCCTGGGCTAATAACAATCATATCGC 1203328
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                                                                                                                                                            Query Match 11.6%;
Best Local Similarity 49.6%;
Matches 683; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
1204379
                                                                              1204439 TAAACATTGAGCTAAATGCGTAAATTCTTCGCCGCGCTTTTCAAAAGAAGCAAACTGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
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ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                       61
GAGACTTGCACAAGCAGGCGACAATAATACCA-----
                     CATGCTAGCACAAGCAGGTGACAAAAGCACACCCTAGCGGTGCTTTGACTGGCTACCAA
                                                                                                            TAPAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC
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                                                                                                                                                                                                                                                                                                      LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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STATE: MD
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INVENTION: The Nucleotide sequence of
the Haemophilus influenzae
Thereof, and Uses Thereof
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                                                                                                                                                         Score 160.4; DB 3; Pred. No. 9.6e-37; 0; Mismatches 606;
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                                                                                                                             GTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTT
                                                                                                                                                                                   TTTTACCATTTGAACCTGTAATCCCCACAATTGGCTTTGTCGCTGCGCGGCA------
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US-10-158-865-1/c
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TITLE OF INVENTION: Thereof, and Uses Thereof
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APPLICANT: Fleischmann et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10158865
Patent No. 6846651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
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CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 09/557,884
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR FILING DATE: 1995-06-07
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NAME/KEY: misc feature
LOCATION: (44416)..(44416)
OTHER INFORMATION: n equal
                                                                   NAME/KEY: misc feature
LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals
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LOCATION: (36636)..(36636)
OTHER_INFORMATION: n equals
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LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals
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LOCATION: (36543)...(36543)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (9921)..(992)
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OTHER INFORMATION: n equals
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NAME/KEY: misc feature
LOCATION: (44975)..(44975)
OTHER INFORMATION: n equal
NAME/KEY: misc_feature
LOCATION: (117136)..(117136)
OTHER_INFORMATION: n equals
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals
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LOCATION: (105121)...(105121)
OTHER INFORMATION: n equals
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LOCATION: (102696)..(102696)
OTHER_INFORMATION: n equals
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LOCATION: (100091)..(100091)
OTHER_INFORMATION: n equals
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LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals
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LOCATION: (51805)...(51805)
OTHER INFORMATION: n equal
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LOCATION: (51786)...(51786)
OTHER_INFORMATION: n equals
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NAME/KEY: (47036)...(47036)
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LOCATION: (45593)...(45593)
OTHER INFORMATION: n equals
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LOCATION: (44905)..(44905)
OTHER INFORMATION: n equal
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LOCATION: (80024)..(80024)
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LOCATION: (65313)..(65313)
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LOCATION: (55369)..(55369)
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LOCATION: (51602)..(51602)
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LOCATION: (51334)..(51334)
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a,
FEATURE:
NAME/KEY: misc_feature
Query Match 11.6%;
Best Local Similarity 49.6%;
Matches 683; Conservative
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
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LOCATION: (145171)...(145171)
OTHER INFORMATION: n equals
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LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals
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LOCATION: (140398)...(140398)
OTHER INFORMATION: n equals a,t,
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals
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LOCATION: (121344)..(121344)
OTHER_INFORMATION: n equals
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LOCATION: (120038)..(120038)
OTHER_INFORMATION: n equals a,t,
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals
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LOCATION: (131360)..(131360)
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LOCATION: (122336). (122336)
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Score 160.4; DB 3;
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                   TTTTACCATTTGAACCTGTAATCCCCACAATTGGCTTTGTCGCTGCGCGCA----
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                                                TCGCTGCCGCAGCTTTTAAGCTATAAGTTGTCTCAAGCTGAAAACTAGAAAGCTCTAGTA
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US-09-543-681A-2830/c
US-09-543-681A-2830/c
; Sequence 2830, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION: NUCLEIC ACID AND AMINO ACITILE OF INVENTION: DIAGNOSTICS AND THERAPEU
; TILE OF INVENTION: DIAGNOSTICS AND THERAPEU
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/9/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 2830
; LENGTH: 1323
; TYPE: DNA
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Best Local Similarity 53.5%;
Matches 352; Conservative
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                       GTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTT
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                                                             TTTTGCCATTAGAGCCTGTTATCGCAACAATAGGTGCTTTTGCCTCACGG
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Pred. No. 1.1e-27;
0; Mismatches 273;
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7702
LENGTH: 1371
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7702
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US-09-252-991A-7702/c
; Sequence 7702, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO PRIVE OF INVENTION: AERUGINOSA FOR DIAGNOSTI FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PRIOR PLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PRIOR DATE: 1998-07-27
NUMBER OF SEQ ID NO 7861
SEQ ID NO 7861
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                                                                                      Query Match
Best Local S
Matches 506
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                        TYPE: DNA
ORGANISM: Pseudomonas
                                                                                                       Local Similarity
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0; Mismatches 500;
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RESULT 10
US-09-701-229-1/c
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; LENGTH: 1450
; TYPE: DNA
; ORGANISM: Pseudomonas
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Best Local Similarity
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CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/087,308
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: PCT/US99/11585
PRIOR FILING DATE: 1998-05-29
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 4
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APPLICANT: Azzolina, Barbara
TITLE OF INVENTION: MURD PROTEIN AND GENE OF
TITLE OF INVENTION: AERUGINOSA
FILE REFERENCE: 20193P
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                                                      GGGGCAACGCTTGTCAGTGTGGTCAAGCATTGCTTGGCTAAATTGGCATCGTCTTTGGTAG 736
                                                                                                                                                                    TGGATTGGTAAAAGTTTGTTTTTTTGATGATATAATGCCATACCATCACCATCATCAAAT
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 ATGATGGCGGTTTGGCCAATTTTCAAAAATACGCAATTTTTGTGCCAAATAATCCACCATG
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Pred. No. 3.8e-25;
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RESULT 11
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5247
LENGTH: 1416
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Best Local Similarity
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ORGANISM: Klebsiella
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CTTTTACCGTTAGAACCGGTAATGGCGATAATCGGCGCCTGCGCTTCGCG------
                                            CCCACGCCGACGTTAACTCCAGCGGCTTTCGCCATCTCGCCCACCAGGGTAGTAACAGTG
                                                                                                                                                                                       CCGACACCAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACAGTG
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Pred. No. 4.1e-20;
0; Mismatches 289;
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US-09-790-988-1
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Best Local Similarity
Matches 289; Conserv
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APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
NOMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: WATANABE, HIDEMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Buchnera
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                                                         CAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTTTGGCGGCGACAATACTCGGCGT 1161
                                                                                                                                                                       GGCGATGATTGGTGTGTTGTTGCTTGAGTTAGATCTCGTGCTTTGAGTGTATCAATGAA
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50.2%;
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Pred. No. 8.4e-14;
0; Mismatches 257;
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                                                                                         US-09-107-532A-1574
Query Match
Best Local Similarity 53.6
Matches 173; Conservative
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1574:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECHONE: (781)893-5007
TELEFAX: (781)893-5277
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                                                                                                           NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...1368
SEQUENCE DESCRIPTION: SEQ ID NO: 157
                                                                                                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                       TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/085,598
FILING DATE: 14 May 1998
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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ADDRESSEE: GENOME THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                    LENGTH: 1368 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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  Score 83; DB 3; Length 1368; Pred. No. 1e-14; 0; Mismatches 150; Indels
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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RESULT 15
US-09-221-017B-881/c
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US-09-252-991A-7787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7787
LENGTH: 567
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7787, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 5.1%; Local Similarity 55.0%;
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                                                                                    502 GCAGCTTGT 510
                                                                                                                                                                                                                                                        382 ACGCCTTCAGCGCGCGAGCATGGCGTCGAACGGCAGGCCGACCGCATGGCCCAGCGCCA
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                                                                                                                            AAAGTTTGT 575
                                                                                                                                                                     GCGCGGCGAGCGCGTTGGAATAGTTGTGGGCGCCACGGATCTTCAGTTCGCCAACCGGCA
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Pred. No. 6.9e-11;
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US-09-221-017B-881
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Best Local Similarity
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                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 09-ARR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY,AGENT INFORMATION:
NAME: MONTOY, Gladys H
REGISTRATION NUMBER: 32,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Ross,
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES
NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2402 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER: PP2911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
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PRIOR APPLICATION DATA:
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ADDRESSEE: MORRISON & FOERSTER
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 1...2402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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OPERATING SYSTEM:
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                                                                                                                                              2165 GGTAGAATTTÁCGTTCGTAGCTTTGGAGTCATTGATATAATCGACACCCTTTACGCGAGC
                                                                                                                                                                 355 GGTTGAGCCGATGTTTGGACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATC
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ATTCTTAATATCCATAGCTTTGGCAGCAATGGCAGTTGCCATAGCATTGTGCCTGTTGTG
                                CATGGGAAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAGGTTATG
                                                                        AATCTTTTCCAGTCGATGCGGTACATTCTTGAAATCCTGCAAGGCTTCTCGAATAGCCTC
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Pred. No. 1.1e-09;
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Search completed: May 18, 2006, 09:34:35 Job time : 268 secs

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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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| EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| FMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
| FMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
| FMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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| FMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
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| FMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
| FMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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   4 10 US-10-958-216-400

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8 4 US-90-754-468-44

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21 9 US-10-158-865-1

10 US-10-981-687-1

4 10 US-10-795-159-685

6 10 US-10-795-159-685

10 US-10-958-216-402

8 US-10-282-122A-30713

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US-10-282-122A-8940

US-09-815-242-7090

US-09-815-242-7090

US-10-282-122A-22236

US-10-988-216-400

US-10-988-216-400

US-11-194-246-220
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Sequence 27195, A Sequence 35, Appl Sequence 7090, Ap Sequence 7090, Ap Sequence 22336, Appl Sequence 20, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 569, App Sequence 685, App Sequence 402, App Sequence 402, Appl Sequence 30713, Ap Sequence 402, App Sequence 40
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Sequence 1, Appli Sequence 21621, A Sequence 37050, A		Sequence 19656, A Sequence 8816, Ap Sequence 30346, A Sequence 41740, A	`` »`	39003, e 25620 e 25077 e 25985	`` »``	5932, 20229, 2, App e 205, e 225,

ALIGNMENTS

APPLICANT: Xu, H.

APPLICANT: Xu, H.

APPLICANT: Xu, H.

APPLICANT: Xu, H.

FILE REFERENCE: ELITRA, 034A

CURRENT APPLICATION INUMBER: U\$/10/282,122A

CURRENT FILING DATE: 2003.02/20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000.03.21

PRIOR FILING DATE: 2000.05.21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000.05.23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000.09.06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/230,347 US-10-282-122A-27195/c
, Sequence 27195, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangeu APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931 APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09 FILING DATE: Ohlsen, Kari Zyskind, Judith Wall, Daniel Trawic. Carr, Grant Carr, Grant Carr, Grant Zamudio, Carlo Malone, Cheryl Yamamoto, Re Forsyth, R. Haselbeck, Robert NUMBER: 60/269,308 2000-12-22 Carlos

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SOFTWARE: PatentIn version 3.1
SEQ ID NO 27195
LENGTH: 1398
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             TGCCCCTTGAGCTGCCAAATTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCAC
                                                                                                                   GGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATTTTTCAAAAATACGCAATTTTTTGTGC
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Sequence 35, Application US/10672787

Publication No. US20040067554A1

GENERAL INFORMATION:
APPLICANT: LAGACE, Robert, E.
APPLICANT: BERG, Kim, L.
TITLE OF INVENTION: NUCLECTION SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REFERENCE: ELITRA.025C1
CURRENT APPLICATION NUMBER: US/10/672,787
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 09/596,002
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL PROGram
SEQ ID NO 35
LENGTH: 96109
TYPE: DNA
ORGANISM: MORAXELLA CATARRHALIS
US-10-672-787-35
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11417 CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA 11476

TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTT

GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA 240 TACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTT 11536 61 CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA 120

1 TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC

TAPAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC 11416

Matches 1380; Query Match Best Local Similarity

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Score 1380; Pred. No. 0; Mismatches

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; ORGANISM: Acinetobacter baumannii
US-10-282-122A-8940
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US-10-282-122A-8940/c
S-10-282-122A-8940/ Application US/10282122A
Sequence 8940, Application US/10282122A
Publication No. US/20040029129A1
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APPLICANT: Wang, Lia
APPLICANT: Zamudio,
APPLICANT: Malone,
APPLICANT: Haselbec
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PRIOR FILLING DATE: 2000-09-06
PRIOR PELICATION NUMBER: 60/230,347
PRIOR PELICATION NUMBER: 60/230,347
PRIOR PELICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 721; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8940
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26
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  GTTGACACAGCTCGACAGCTTCTTTAAGCGTTGCTGCATGTAAAATTTTAGTTGCGCCT-
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Zyskind, Judith
Wall, Daniel
Trawick, John
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                                        ACTGCCCGATCAAGTGTACCAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTTG 181
                                                                                                                        ATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAAT
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Vamamoto, Robert
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Malone, Cheryl
Haselbeck, Robert
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                                                                                                     TCGGCTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGC 125
                                                                                                                                                                   GCAATAGCTGCCTGAATTTCCGGTAATTGTGGTGCAAGGCCCTGGGCTTAAAATAATCTCT
                                                                                                                                                                                                                            GCTTTGGCCGCCGACAATACTCCGCCGTTCTTGGGTTAATGCCCGGGGCTGATGATCATCTGA 1195
                                                                                                                                                                                                                                                                                    -----ACGACGCAATAATTGGATATCACCCACACAGAAATACCTTTA
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APPLICANT: Yamamoto, Robert T.

APPLICANT: Yamamoto Modert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Es

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION UNMBER: US/09/815,24

CURRENT FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7090
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Patent No. US2002006
GENERAL INFORMATION:
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Best Local Similarity
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Haemophilus influenzae FEATURE:
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LOCATION: (1)
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                                                                                                           GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA
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Pred. No. 2.1e-33;
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                                                                                                          TATCAATACCAGTAGGATTTTTTCGAGTATCAATCACACGAATATTAGCCTGTTGGGATA
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AGAGATAATCCACACAAGAAAGACCTGTTTTGCCCAAGCCCGATGATAGTAATATTTTT
                                                                                                                                                           TATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGATTGA 1319
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,337
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
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US-10-282-122A-22236/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22236
LENGTH: 1314
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Publication No. US20040029129A1
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
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APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
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                                                                 GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA
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                                                                                                                                                                                               GAGACTTGCACAAGCAGGCGACAATAATACCA----
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  CTGCATAACATATGCTGACAGCTCACTAAAATCTTGACCTTTACCAAGCCCAACCCAAAAT 300
                                        CGATGAAAATTTTTGCAAGCAGCGCACCATCTCGACCAAAACAATAACAAATAATGTGTGG
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Carr, Grant
Carr, Robert
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Forsyth, R.
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Ohlsen, Kari
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ilarity 49.6%;
Conservative
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Pred. No. 2.1e-33;
0; Mismatches 606;
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TATCTGCCAAGGTAGGATTGGGATTACCATCGATGATGCTAACTTTGTGACCGTGATTGA 1319
                                                                                                                                                                                     TTTCAAGTAACCATTCCTGATTTAAACTACCAGTATGAAGAGGGATATTTTGAGGAAGTT 137
                                                                                                                                                                                                                              CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGCAGTT 1259
                                                                                                                                                                                                                                                                                          GTGCGGTTTGAATTTCTGGTGTTTTTACCGCAAGCCCTGGGCTAATAACAATCATATCGC 197
                                                                                                                                                                                                                                                                                                                                     TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGG 1199
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                                                                                 TATCAATACCAGTAGGATTTTTTCGAGTATCAATCACACGAATATTAGCCTGTTGGGATA 77
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Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 1132
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 400
LENGTH: 1314
TYPE: DNA
ORGANISM: Haemophilus influenzae
US-10-958-216-400
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US-10-958-216-400/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/958,216
CURRENT FILING DATE: 2004-10-04
PRIOR APPLICATION NUMBER: PCT/CA03/00462
PRIOR FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: 60/369,511
PRIOR APPLICATION NUMBER: 60/385,089
PRIOR APPLICATION NUMBER: 60/385,089
PRIOR APPLICATION NUMBER: 60/385,751
PRIOR PILING DATE: 2002-05-31
PRIOR PILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 60/385,751
PRIOR APPLICATION NUMBER: 60/386,553
PRIOR FILING DATE: 2002-06-04
PRIOR FILING DATE: 2002-06-05
PRIOR FILING DATE: 2002-06-05
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PRIOR PILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/386,566
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/386,390
PRIOR APPLICATION NUMBER: 60/386,601
PRIOR APPLICATION NUMBER: 60/386,601
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
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Query Match
Best Local Similarity
Matches 683; Conserv
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APPLICANT: VIRAG, CRISTINA
TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES
FILE REFERENCE: IPT-205.01
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APPLICANT: DHARAMSI, AKIL
APPLICANT: VEDADI, MASQUD
APPLICANT: ALAM, MUHAMMAD ZAHOOR
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CANADIEN, VERONICA
DOMAGALA, MEGAN
HOUSTON, SIMON
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PINDER, BENJAMIN
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MCDONALD, MERRY-LYNN
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LI, QIN
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  Conservative
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Score 160.4; DB 10;
Pred. No. 2.1e-33;
0; Mismatches 606;
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TGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATCTGATCGG 1199
                                                                                                                              GTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTT
                                                                                                                                                                                                                                            CGACACCAACAATCATGCCTGCATGTTTTGCCATCTCGCCTACTAATGTCGTAACAGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGATTGGCAGCTGTGCCTAAGGCAAGTGCAGATAAGGCATTGAGTAGGTTATGCTTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGATGAAAATTTTGCAAGCAGCGCACCATCTCGACCAAAAACAATAACAAATAATGTGTGG 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA 240
                                                                                                                                                                                                                                                                                                                                       CCATACCAACTTTCACACCAGCAGCTTTCGCCATTTCATAAACTAAAGTAGTTACGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATAAAGTTCACAATCTTCATTC---AACAATGACAAAGCGGGAATCCCAATATTTCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTTGGGCGTAAAAATTCTATCGCTTGTTCCATTGTATCGAACAA-----ATAACTTTG 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGACTTGCACAAGCAGGCGACAATAATACCA---
                                                                                                                                                                                                        TTTTACCATTTGAACCTGTAATCCCCACAATTGGCTTTGTCGCTGCGCGGCA-----
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                                                                  ----GAATAATTCAATATCGCCGATTACTTCCACTCCCGCTTTAA
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APPLICANT: Nott, John
APPLICANT: Trepod, Catherine
APPLICANT: Trepod, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND METH.
TITLE OF INVENTION: USE
FILE REFERENCE: 00592.US1 (M&R 268.05920101)
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR APPLICATION NUMBER: US/0/274,586
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2002-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: Patentin version 3.0
SEQ ID NO 220
LENGTH: 2925
TYPE: NUMBER: 025
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US-11-194-246-220/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 220, Application US/11194246 Publication No. US20050272089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: ARTIFICIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 11.6%;
Local Similarity 49.6%;
                                                                  1958
                                                                                                                                                                                                                                           2078
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                                                                                                                                                        2018 TTGATTAATTTAATTCAGCTAATTCTGAAAAATCAGCCCCTTTTCCGTCTCCGCCTAGCAA 1959
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361 GCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATCATCAATATA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CATGCTAGCACAAGCAGGTGACAAAAGCACAGCCCTAGCGGTGCTTTGACTGGCTGCCAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TAAAGCGTGAACCATGTTAACAAACTTATCACCTCGCTCATTATAATTTTTAAATTGATC
                                                                  CÁAATGCAATTTACCCTCAATATÁ------AAGCCCAGCCAATGCAGCAACTGTACT 1908
                                                                                                                                                                                      CGATGAAAATTTTTGCAAGCAGCGCACCATCTCGACCAAAACAATAACAAATAATGTGTGG
                                                                                                                                                                                                                                                                                    GAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAATACACACTATCCACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                          GAGACTTGCACAAGCAGGCGACAATAATACCA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGACGCATATTTTT 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGCAGTT 1259
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                                                                                                            CAATGCCAGTGATGATATGCCATAAACCGTGCCAAGCCCCATCAATTGCTGCAATGGTTGA 360
                                                                                                                                                                                                                                                                                                                                TGTTGGGCGTAAAAATTCTATCGCTTGTTCCATTGTATCGAACAA----ATAACTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 160.4; DB 15;
Pred. No. 3.4e-33;
0; Mismatches 606;
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RESULT 8
US-09-754-468-44/c
US-09-754-468-44/c
; Sequence 44, Application US/09754468
; Publication No. US20050192237A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCCTTGAGCTT
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                                                                                                                                                                AGAGATAATCCACACAAGAAAGACCTGTTTTGCCAAGCCCGATGATAGTAATATTTTT
                                                                                                                                                                                                 CCAAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGGCATATTTTTT 1377
                                                                                                                                                                                                                                            TATCAATACCAGTAGGATTTTTTCGAGTATCAATCACACGAATATTAGCCTGTTGGGATA 1009
                                                                                                                                                                                                                                                                                                                                                               CTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACAATGAACGCCTGTGGGCAGTT 1259
                                                                                                                                                                                                                                                                                                                                                                                                      GTGCGGTTTGAATTTCTGGTGTTTTTTACCGCAAGCCCTGGGCTAATAACAATCATATCGC
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FILTE OF INVENTION: Composition and Method

FILE REFERENCE: 0450-0033.30

CURRENT APPLICATION UMBER: US/09/754,468

CURRENT FILING DATE: 2001-01-04

PRIOR APPLICATION NUMBER: US 60/174,484

PRIOR FILING DATE: 2000-01-04

INUMBER OF SEQ ID NOS: 112

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 44
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Matches 683; Conserv
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Best Local S
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TYPE: DNA
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                                                                                                                                                                                                                                                                                  SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn vers
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/329,670 CURRENT FILING DATE: 2002-12-24 PRIOR APPLICATION NUMBER: US 9/643,990 PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae TITLE OF INVENTION: Thereof, and Uses Thereof FILE REFERENCE: PB186P1
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                                   FEATURE:
NAME/KEY: misc feature
LOCATION: (9921)..(9921)
OTHER INFORMATION: n equals
FEATURE:
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LOCATION: (4747)..(4747)
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ORGANISM: Haemophilus influenzae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (10150)..(10150)
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FEATURE:
NAME/KEY: misc feature
ΓΩΛΉΤΟΝ: (55369)..(55369)
NAME/KEY: misc feature
LOCATION: (653\overline{\overline{1}}3)...(65313)
OTHER INFORMATION: n equals
                                                                                          NAME/KEY: misc feature
LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: (51805)..(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(5180T)...(518
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LOCATION: (51602)...(51602)
OTHER INFORMATION: n equals
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LOCATION: (45732)...(45732)
OTHER INFORMATION: n equals
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LOCATION: (51786)..(51786)
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals
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LOCATION: (47036)..(47036)
OTHER INFORMATION: n equal
FEATURE:
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LOCATION: (45593)..(45593)
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LOCATION: (44416)..(44416)
OTHER INFORMATION: n equals
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NAME/KEY: (40808) . (40810)
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LOCATION: (36636)..(36636)
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LOCATION: (36543)...(36543)
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LOCATION: (29298)..(29
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NAME/KEY: misc_feature
LOCATION: (142750)...(142750)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (145058)...(145058)
OTHER INFORMATION: n equals a,
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LOCATION: (100091)..(100091)
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LOCATION: (105121)...(105121)
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LOCATION: (80024)..(80024)
OTHER_INFORMATION: n equals a,
                                                                                                     NAME/KEY: misc_feature
LOCATION: (140398)..(140398)
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LOCATION: (139910)..(139910)
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LOCATION: (131360)..(131360)
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LOCATION: (131340)..(131340)
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LOCATION: (122336)..(122336)
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LOCATION: (122167)...(122167)
OTHER INFORMATION: n equals
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LOCATION: (121344)...(121344)
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LOCATION: (120038)..(120038)
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LOCATION: (119924)..(119924)
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LOCATION: (119750)..(119750)
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LOCATION: (117136)..(117136)
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LOCATION: (107248)..(107248)
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LOCATION: (102696)..(102696)
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals
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LOCATION: (145171)...(145171)
OTHER INFORMATION: n equals
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LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals
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(152530)..(152530)
TGATAATGGTGTGATTTGGGGGCAACGCTTGTCAGTGTGGTCAAGCATTGCTTGGCTAAAT
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TRACCATTATGATAAATCGTAAATTTGCTT ICCAAGATGATCATCAGCGGAGAGATTTAAAATTG ICCATATGATCTCAGCGGAGAGATTTAAAATTG ICCCATATGATCTTCAGTCAGCGTCAAGACAG ICCCTCAAGCTGAAAACCTGACAGCTCAAGCA AATTCAAGCTGAAAACCTGACAATATTACCGC AATTCAAGCTGAAAACCTAAATGTCGAATATTACCGC SCCATTTCCATACTAAATGTCGAATATTTCCGC	INGCAATTTTCAAAAATACCCAATTTTTG	RESULT US-10-1 ; Seque ; Seque ; Dendi ; GENEE ; APPL ; TITI ; TILL ; FILL ; PRIC ; PR	g Q	8 8 8 8	8 8 8 8	8 8 8 8	D Q D Q D Q
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OTHER INFORMATION: n equals a,t,c, or g
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.786)..(51786)
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5732)..(45732)
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1905)..(44905)
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(416)..(44416)
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5551)..(36551)
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369)..(55369)
TION: n equals a,t,c, or g
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334)..(51334)
TION: n equals a,t,c,
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593)..(45593)
TION: n equals a,t,c,
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636)..(36636)
TION: n equals a,t,c,
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543)..(36543)
TION: n equals a,t,c,
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298)..(29298)
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036)..(47036)
TION: n equals a,t,c,
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975)..(44975)
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308)..(40810)
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FEATURE:

NAME/KEY: misc_feature
LOCATION: (139910)..(139910)

OTHER INFORMATION: n equals
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LOCATION: (131360)..(131360)
OTHER INFORMATION: n equals
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LOCATION: (100091)..(100091)
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LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (131340)...(131340)
OTHER INFORMATION: n equals
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LOCATION: (122336)..(122336)
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LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals
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LOCATION: (121344)..(121344)
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LOCATION: (120038)..(120038)
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LOCATION: (119324)..(119924)
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LOCATION: (119750)..(119750)
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LOCATION: (117136)..(117136)
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals
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LOCATION: (105121)..(105121)
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LOCATION: (102896)..(102696)
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Best Local Similarity 49.6%;
Matches 683; Conservative
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NAME/KEY: misc_feature
LOCATION: (152530)..(152530)
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LOCATION: (150841)..(150841)
OTHER_INFORMATION: n equals
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LOCATION: (147197)...(147197)
OTHER INFORMATION: n equals
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LOCATION: (145942)..(145942)
OTHER_INFORMATION: n equals
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LOCATION: (145171)...(145171)
OTHER INFORMATION: n equals
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals
FEATURE:
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OTHER INFORMATION: n equals
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Pred. No. 1.4e-31;
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US-10-981-687-1/c
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Publication No. US20050131222A1
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.

TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae in Interest.

TITLE OF INVENTION: Thereof, and Uses Thereof.

FILE REFERENCE: PB186P2C1D12

CURRENT APPLICATION NUMBER: US/10/981,687

CURRENT FILING DATE: 2004-11-05

PRIOR APPLICATION NUMBER: US 10/158,865

PRIOR FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: US 09/557,884

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 08/476,102

PRIOR APPLICATION NUMBER: US 08/476,787
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NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.:
SEQ ID NO 1
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LOCATION: (40808)...(40810)
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LOCATION: (102696)..(102696)
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LOCATION: (150841)..(150841)
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LOCATION: (147197)...(147197)
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NAME/KEY: misc_feature

LOCATION: (145942)..(145942)

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Sequence 569, Application US/10795159
Publication No. US20050221439A1
GENERAL INFORMATION:
APPLICANT: BAKALETZ et al.
TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE
FILE REFERENCE: 28335/38815A
CURRENT APPLICATION NUMBER: US/10/795,159
CURRENT FILING DATE: 2004-03-05
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                                                                        ATTTCCGCCCATACCAACTTTCACGCCAGCAGCTTTCGCCATTTCATAAACTAAAGTAGT
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nes 591; Conservative 0; Mismatc 172 ATCACCTTTGAGTAAATCTTGCTCAATTAT	11.2%; Score 154.4; l larity 49.0%; Pred. No. 4.4e.	NAME/KEY: misc feature ; NAME/KEY: misc feature ; LOCATION: (908604)(908641) ; OTHER INFORMATION: n is a, c, g, or t	NAME/KEY: misc feature LOCATION: (292495)(292495) OTHER INFORMATION: n is a, c, g, or t	; NAME/KEY: misc feature ; NAME/KEY: misc feature ; LOCATION: (292404)(292404) ; OTHER INFORMATION: n is a, c, g, or t	NAME/KEY: misc feature ; NAME/KEY: misc feature ; LOCATION: (39640)(39640) ; OTHER INFORMATION: n is a, c, g, or t	; NAME/KEY: misc feature; LOCATION: (9223); LOCATION: (9223); OTHER INFORMATION: n is a, c, g, or t	; EEQTID NO 683 ; LENGTH; 908766 ; TYPE: DNA ; ORGANISM: H. influenzae		FILE REFERENCE: 2838/38815A CURRENT APPLICATION NUMBER: US/10/795,159 CURRENT FILING DATE: 2004-03-05-05 CURRENT FILING DATE: 2004-03-05-05	PI OPINIO MININA TOLINIA DI MOMBILITA IL	RESULT 13 US-10-795-159-685/c	Qy 1372 TTTTT 1377 Db 6411 ATTTT 6416	Qy 1312 GTGATTGACCAAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGACGACGACGACGACGACGACGACG	Qy 1252 GGGCAGTTTATCTGCCAAGGTAGGATTGGGATTGCGATGGATG	Qy 1192 CTGATCGGCTGAGCTTAAGAGTTCACTGTCCAAGCTGCCAAAATGACGAAGGAATGAACGCCTGT 1251	Qy 1132 TTGAGCTTTGGCGGCGACAATACTCGGCGTTCTTGGGTTAATGCCGGGGCTGATGATGATGAT 1191	QY 1072 TAGATCTCGTGCTTTGAGTGTATCAATGAACAATTGAACATCGCTGATCACAGGAATGCC 1131
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; TYPE: DNA
; ORGANISM: Legionella pneumophila
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25165
LENGTH: 1281
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
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APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-10-23
                                                         1103 GAACGAACAAATTCTGAAACTGGCTGGGCTAATTCTTGGAAATCCGCCCCTTTTCCCTGT
                                                                                                                                                                                                               464;
                                                                                                                                                               170 GCATCACCITTGAGTAAATCTTGCTCAATTATCGGGGCATCTTGACCGATTAAAATACACA
CCACCCAAAATCAATGCCAGTGATGATATGCCATAAACCGTGCCAAGCCCCATCAATTGCT
                                                                                           CTATCCACCCACTGCATAACATATGCTGACAGCTCACTAAAATCTTGACCTTTACCAAGC
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Pred. No. 2.8e-31;
0; Mismatches 412;
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US-10-958-216-402/c RESULT 15 Sequence 402, Application US/10958216 Publication No. US20050181388A1 GENERAL INFORMATION: APPLICANT: APPLICANT: APPLICANT: EDWARDS, ALED APPLICANT: DHARAMSI, AK APPLICANT APPLICANT APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: VEDADI, MASOUD ALAM, MUHAMMAD ; ARROWSMITH, CHEI MANSOURY, KAMRAN MCDONALD, MERRY-LY NETHERY, KATHLEEN NG, IVY BUZADZIJA, KRISTINA CANADIEN, VERONICA DOMAGALA, MEGAN KANAGARAJAH, DHUSHY HOUSTON, AWREY, DONALD E. BEATTIE, BRYAN QIN , MERRY-LYNN KATHLEEN SIMON AKIL CHERYL ZAHOOR

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APPLICANT: VIRAG, CRISTINA
TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FRO
FILE REFERENCE: IPT-205.01
FILE REFERENCE: IPT-205.01
CURRENT APPLICATION NUMBER: US/10/958,216
CURRENT FILING DATE: 2004-10-04
PRIOR APPLICATION NUMBER: ECT/CA03/00462
PRIOR APPLICATION NUMBER: 60/369,511
PRIOR APPLICATION NUMBER: 60/385,089
PRIOR FILING DATE: 2002-04-02
PRIOR FILING DATE: 2002-05-31
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: 60/385,751
PRIOR APPLICATION NUMBER: 60/386,553
PRIOR APPLICATION NUMBER: 60/386,553
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/386,577
PRIOR APPLICATION NUMBER: 60/386,577
PRIOR APPLICATION NUMBER: 60/386,567
PRIOR APPLICATION NUMBER: 60/386,567
PRIOR APPLICATION NUMBER: 60/386,566
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TYPE: DNA
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US-10-958-216-402
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Best Local Similarity 49.2%;
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SEQ ID NO 402
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PRIOR APPLICATION NUMBER: 60/386,601
PRIOR FILING DATE: 2002-06-06
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Pred. No. 3.7e-31;
0; Mismatches 611;
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                                                                                                                                     TTTCAAGTÁACCATTCCTGATTTÁAACTACCAGTÁTGÁAGÁGGGÁTATCTTGAGGAAGTT 137
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                             CCAAAAATTCACAGCTGACAGTCCAGAGCTGCCCAAACCGACGACGGCATATTTTTT 1377
                                                                  TATCAATACCAGCAGGATTTTTTCGAGTATCAATCACACGAATATTAGCCTGTTGGGATA
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Search completed: May 18, 2006, 10:00:18 Job time : 1704 secs

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Result
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| MMC_Celerra_SIDS3/ptcdata/1/pubpna/US09_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptcdata/1/pubpna/US07_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptcdata/1/pubpna/US07_NEW_PUB.seq:*
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                                                                         Sequence 118, App Sequence 2634, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3775, Appli Sequence 3776, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16180, Sequence 7811, Appli Sequence 7812, Appli Sequence 7815, Appli Sequence 3845, Appli Sequence 3845, Appli Sequence 3845, Appli Sequence 3846, Appli Sequence 7246, Appli Sequence 7251, Appli Sequen
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Sequence 80706, A
Sequence 4664, Ap
Sequence 23, Appl
                       RESULT 2
US-11-217-529-2634/c
(S-11-217-529-2634, Application US/11217529
; Sequence 2634, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
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APPLICANT: SUNTORY LIMITED

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	217529 O R ANALYZING GENES OF /11/217,529 0/932,182 orianus rianus Score 34.2; DB 7; Pred. No. 0.42;	US-11-217-529-3737 US-11-217-529-79615 US-11-217-529-5615 US-11-488-619-1129 US-10-488-619-2704 US-10-488-619-1435 US-10-488-619-1436 US-10-488-619-1434 US-10-488-619-1434 US-10-488-619-1434 US-11-218-64 US-11-233-726-4 US-11-217-529-2417 US-11-217-529-2417 US-11-217-529-2417 US-11-217-529-1751 US-11-217-529-1751 US-11-217-529-2728 US-10-505-928-151
INGELS 0; Gaps 0; rGGCAGCTGTGCCTAAGGCA 505 ATTATTC 981	INDUSTRIAL YEASTS	Sequence 3737, Ap Sequence 79615, Ap Sequence 5615, Ap Sequence 1129, Ap Sequence 1139, Ap Sequence 1398, Ap Sequence 1138, Ap Sequence 1134, Ap Sequence 1424, Appli Sequence 42, Appli Sequence 2465, Ap Sequence 2417, App Sequence 2728, App Sequence 1751, App

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                   SEQ ID NO 2
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LENGTH: 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: EX03-003C-PC CURRENT APPLICATION NUMBER: US/10/504,120 CURRENT FILING DATE: 2004-08-06 PRIOR APPLICATION NUMBER: 60/354,824 PRIOR FILING DATE: 2002-02-06 PRIOR APPLICATION NUMBER: 60/358,217 PRIOR APPLICATION NUMBER: 60/358,217 PRIOR FILING DATE: 2002-02-02
                                      Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 32 SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Exelixis, Inc.
TITLE OF INVENTION: MINRS AS MODIFIERS OF INSULIN RECEPTOR SIGNALING AND METHODS
TITLE OF INVENTION: USE
                                                                                                                PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2002-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: S-38-285
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APPLIÇANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Match 2.4%;
Local Similarity 51.0%;
les 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/358,126 FILING DATE: 2002-02-20
                                                                                                                                                           APPLICATION NUMBER: 60/360,222 FILING DATE: 2002-02-26
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FILING DATE: 2002-02-21
APPLICATION NUMBER: 60/358,765
FILING DATE: 2002-02-21
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FILING DATE: 2002-02-21
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                                                                                                                                                                                                       APPLICATION NUMBER: 60/359,531 FILING DATE: 2002-02-25
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3411
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                                                                                      See File Wrapper or
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US-11-217-529-77328/c

Sequence 77328, Application US/11217529 Publication No. US20060099612A1 GENERAL INFORMATION:

APPLICANT: SUNTORY LIMITED APPLICANT: NAKAO, YOSHIHI APPLICANT: NAKAMURA, NORI

YOSHIHIRO RA, NORIHISA

RESULT 5

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CURRENT FILING DATE: 2005-11-09
PRIOR APPLICATION NUMBER: US/09/369,992
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: PCT/IB98/00212
PRIOR FILING DATE: 1998-02-05
PRIOR PPLICATION NUMBER: AU P09481/97
PRIOR PILING DATE: 1997-09-26
PRIOR PILING DATE: 1997-09-26
PRIOR FILING DATE: 1997-09-26
PRIOR APPLICATION NUMBER: AU P09329/97
PRIOR FILING DATE: 1997-04-21
PRIOR APPLICATION NUMBER: AU P09329/97
PRIOR FILING DATE: 1997-04-21
PRIOR APPLICATION NUMBER: AU P0933/97
PRIOR FILING DATE: 1997-04-21
PRIOR APPLICATION NUMBER: AU P04953/97
PRIOR FILING DATE: 1997-02-06
                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver.
SEQ ID NO 3
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Publication No. US20060099627A1
GENERAL INFORMATION:
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                                                                                                                                              Matches
                                                                                                                                                                                 Query Match
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APPLICANT:
APPLICANT:
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APPLICANT: Ting, Robert C.
APPLICANT: Tham, Jilm.
                                                                                                                                                                                                                                                         LENGTH: 51
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Diagnosis of Parasites FILE REFERENCE: 64-99
                                                                                                                                                                                                                                        ORGANISM: Plasmodium berghei
                                                                                                                                                                 Local Similarity
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                                 141 CAACCTGATATATTTTAGATGCCAAATGTGCATCACCTTTGAGTAAATCTTGCTCAATTA
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Nelson, James S. Tan, Theresa M.
                                                                                                                                              Conservative
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                                                                                                                                            Score 31.8; DI
Pred. No. 1.3;
0; Mismatches
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Pred. No. 2
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APPLICANT: NAKAMÜRA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, TOKIKO
APPLICANT: KODAMA, TOKIKO
APPLICANT: ASHIKARI, TOSHIHIKO
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT APPLICATION NUMBER: US 10/932,182
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR APPLICATION USBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PAECHLIN VETBION 3.3
SOFTMARE: PAECHLIN VETBION 3.3
SOFTMARE: PAECHLIN VETBION 3.3
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; ORGANISM: Saccharomyces pastorianus US-11-217-529-77328
                                                                                                                                                                                                                                                                                                                                      APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHHIRK
APPLICANT: NAKAMURA, NORIH;
APPLICANT: KODAWA, YUKIKO
APPLICANT: FUJIMURA, TOMOKK
APPLICANT: ASHIKARI, TOSHII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Publication No. US20060099612A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 147; Conserv
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APPLICANT: ASHIKARI, TOSHHHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 10/932,182 PRIOR FILING DATE: 2004-09-02
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NAME/KEY: modified base LOCATION: (358)..(385) OTHER INFORMATION: a, c,
                                                                                 TYPE: DNA ORGANISM: Saccharomyces pastorianus
                                                                   FEATURE:
                                                                                                                            ENGTH:
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ilarity 43.4%;
Conservative
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  t, unknown, or other
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Pred. No. 2.5;
0; Mismatches 192;
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US-11-217-529-3776/c
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                                                           Sequence 16, Application US/10504120 Publication No. US20060088829A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.3
SEQ ID NO 3776
LENGTH: 1125
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Best Local
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CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
APPLICANT: Exelixis, Inc.
TITLE OF INVENTION: MINRS AS MODIFIERS OF INSULIN RECEPTOR SIGNALING AND METHODS OF
TITLE OF INVENTION: USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
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APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SUNTORY LIMITED APPLICANT: NAKAO, YOSHIHII APPLICANT: NAKAMURA, NORII APPLICANT: KODAMA, YUKIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: modified base
LOCATION: (94)..(121)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Saccharomyces pastorianus
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                                                                                                                                                                                                                             ATCAATATATTCACAGCGATGCGGTAGCCCTTTGAAAGTCTTAAGG
                                                                                                                                                                                                                                                                                                  AATGGTTGAGCCGATGTTTGTACCTTTTGAATCATTAAAATATGCCTTGCTATCAATATC
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                                                                                                                                                                                            ATTCAGTTCAATAAAGTGATTCATTCCTTGTATTACGGCCATATGG
                                                                                                                                                                                                                                                                 ATTGTTTTCATCTATGTATGTATCATCTGAATCAGCTGAATGCGTCTGGAATGCTTTATC
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NAKAMURA, NORIHISA
KODAMA, YUKIKO
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Pred. No. 2.4;
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Pred. No. 2;
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REFERENCE: EX03-003C-PC

US/10/504,120

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US-11-217-529-166180/c
Sequence 166180, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-504-120-16
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PRIOR FILING DATE: 2002-02-20
PRIOR PELICATION NUMBER: 60/358,126
PRIOR APPLICATION NUMBER: 60/358,95
PRIOR APPLICATION NUMBER: 60/358,95
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/358,756
PRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
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Matches
                    Query Match
Best Local (
                                                                                                                                                   SEQ ID NO 166180
LENGTH: 5026
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                                                                                                                                                                                          FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                              APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/360,222
PRIOR TILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 60/360,224
PRIOR FILING DATE: 2002-02-26
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                                                                                                       ORGANISM: Saccharomyces pastorianus
                                                                                                                                 TYPE: DNA
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ETILING DATE: 2002-02-21
APPLICATION NUMBER: 60/359,531
FILING DATE: 2002-02-25
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68;
                    Similarity
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Similarity 56.2%;
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Conservative
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                  2.3%;
Score 31.4; D
Pred. No. 6.2;
0; Mismatches
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                                       DB 7;
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61;
                                         Length 5026;
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Gaps
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APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
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CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
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                                                                                                                                                            APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
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APPLICANT: ASHIKARI, TOSHIHIKO
TITILE OF INVENTION: METHODS FOR ANALYZING
FILE REFERENCE: S-38-285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.3
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Local Similarity 50.0%;
hes 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                TTTTCTTTTCCATTTCCAAAAGTTTCTTTCTTTGCT 479
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NAKAMURA, NORIHISA
KODAMA, YUKIKO
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                                                                                                       OF INDUSTRIAL
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RESULT 13
US-11-217-529-4571/c
JS-10-217-529-4571/c
JS-20060099612A1
GENERAL INFORMATION:
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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1381
                                                                                                                                                                                                                                                                                                                                             US-11-217-529-76422
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APPLICANT: FUJMURA, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 76422
LENGTH: 2385
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKANURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3
SEQ ID NO 1381
LENGTH: 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 76422, Application US/11217529 Publication No. US20060099612A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 102;
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                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Saccharomyces pastorianus
                                                                                                                                                                                                                                                                                    Match 2.3%;
Local Similarity 63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 637 GTGGCTAAGTAAGCTATTTGTTGTGATAATGGTGTGATTTGGGGGCAACGCTTGTCAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       577 TTTTTGATGATAATGCCATACCATCACCATCAAATAAAATAAAATCTGCCGTTTG
                                                                                                                                                             607 ATCATCAAATAAATAA 622
                                                                                                                                                                                                                             909 TTCCANAGACGATAGGTTTCTTAAGAGATCATGCAACATG 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            969 ATTCCAAATGTTATTGGTAAGTGTTGTCAATTCTTGAGAGTTAAAAGTGTTTATAATTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             697 GGTCAAGCATTGCTTTGGCTAAATTGGCATCGTCTTGGTAGATGATGGCGGTTTGGCAATT
                                                                                                                                                                                                                                                                       48;
                                                                                                                                ATAATGTGTTGAATAA
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                                                                                                                                                                                                                                                                                                       DB 7;
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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4571
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CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
PRIOR SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4571
LENGTH: 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 80459, Application US/11217529 Publication No. US20060099612A1 GENERAL INFORMATION:
                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.3 SEQ ID NO 80459
                                                                                                                                              Matches
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APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHLRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
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APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Saccharomyces pastorianus
                                                                                                                                                                                                                                                                            LENGTH: 1593
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                                  917 TGGATCGTTAATAATTCAAGTGCAGGCGTGCCAAT 951
                                                                       662 ÁÁTTGTGÁAÁCGTGGGACTGGATCAAÁCTTGAAÁGATCAACGGCATCCATATCCATATTG
                                                                                                        857 AAATTTGAGATATGCTCAAGCTGAAAACTTGACAGCTCAAGCACCACCAAATCCATATTT
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KODAMA, YUKIKO
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NAKAMURA, NORIHISA
                                                                                                                                            Conservative
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Pred. No. 4.4;
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Pred. No.
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                                                                                                                                              Indels
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RESULT 15 US-11-217-529-78136/c ; Sequence 78136, Application US/11217529

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GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION UNMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NO%: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 78136
LENGTH: 1125
TYDE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-78136
Search completed: May 18, 2006, 11:42:15 Job time : 52 secs
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                                                                                        364 ATAAAAAAATCGTTCATAAAT 343
                                                                                                                                                                                                                 638 TGGCTAAGTAAGCTATTTGTTGTGATAATGGTGTGATTTGGGGGCAACGCTTGTCAGTGTG 697
                                                                                                                                                                                                                                                                                                                                                         544 GCATTTTATAGCATTGCCTTTCGTTGAACATTTTTTGAATTTTTTCGTGATACTCTGCAT
                                                                                                                                698 GTCAAGCATTGCTTGGCTAAAT 719
                                                                                                                                                                              424 TGCTGAAGTCAATTTTAAAGTATGATAATGCTATTCTTATTCTTTTGGTATTGTTCATCTA 365
                                                                                                                                                                                                                                                                     484 TTCCTTCTTTACAATTAATCAAGTTTTCAACCAATAACTTCAATAAATCATTCAGAGACG
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